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KIM MARSHALL
MANAGER EXAMINATION SUPPORT AND
SALES





AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

P. gingivalis antigens

The invention is described in the following statement:

M1034 55 0 4 AUG98

P. gingivalis antigens

FIELD OF THE INVENTION

5 The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*.

BACKGROUND OF THE INVENTION

10 Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated
15 with a subgingival infection of a consortium of specific Gram-negative bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically
20 cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of
25 the disease. The progression of periodontitis lesions in non-human primates has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

P. gingivalis is a black-pigmented, anaerobic, asaccharolytic,
30 proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence
35 factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*. The DNA sequences listed below have been selected from a

large number of *P. gingivalis* sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the *P. gingivalis* DNA sequences to the known protein sequence databases. Some of the characteristics used to
 5 select useful vaccine candidates include; the expected cellular location, such as outer membrane proteins or secreted proteins, particular functional activities of similar proteins such as those with an enzymatic or proteolytic activity, proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism, proteins
 10 that might be expected to play a role in the pathogenesis of the organism eg. red cell lysis, cell agglutination or cell receptors and proteins which are paralogues to proteins with proven vaccine efficacy. DNA sequences that were considered to be poor vaccine candidates and not selected include those that code for proteins involved in replication, non-essential proteins
 15 involved in cellular processes and those proteins present at sites that would be unlikely to be affected by immune mediators such as those found in the bacterial cytoplasm or inner membranes.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or
 20 including a sequence selected from the group consisting of SEQ ID NO: 1 to 44, fragments thereof and sequences complementary thereto.

In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group
 25 consisting of SEQ ID NO: 1 to 44, fragments thereof and sequences complementary thereto.

In a third aspect the present invention consists in an isolated *P. gingivalis* polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 45 to 137 or fragments
 30 thereof.

In a fourth aspect the present invention consists in an isolated polynucleotide, the polynucleotide encoding a polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 45 to 137 or fragments thereof.

35 In a fourth aspect the present invention consists in a nucleotide probe specific for *P. gingivalis*, the probe including a detectable label and a

nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting SEQ ID NO: 1 to 44 and sequences complementary thereto.

5 In a fifth aspect the present invention consists in a composition for use in raising an immune response in an animal directed against *P. gingivalis* the composition including an acceptable carrier and/or adjuvant and at least one polypeptide having a sequence selected from the group consisting of SEQ ID NO: 45 to 137 or fragments thereof.

10 As will be understood by those skilled in the art the nucleotides of the present invention may be useful in DNA vaccination to reduce the incidence and/or severity of *P. gingivalis* infection.

Accordingly in a sixth aspect the present invention consists in a composition for use in inducing an immune response, the composition including at least one DNA molecule, the at least one DNA molecule having or including a sequence selected from the group consisting of SEQ ID NO: 1
15 to 44, fragments thereof and sequences complementary thereto.

Further information regarding DNA vaccination may be found in Donnelly *et al*, Journal of Immunological Methods 176(1994) 145-152, the disclosure of which is incorporated herein by reference.

20 Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

25

DETAILED DESCRIPTION

Preparation of the *P. gingivalis* library for sequencing.

30 To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (1961)(1). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (1995)(2). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA
35 and was treated with Bal31 nuclease to create blunt ends then run twice on preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from

the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed on a 1% agarose preparative gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated
 5 to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates
 10 containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

15 DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a
 20 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing
 25 primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems). Raw trace data files from the ABI 377 sequencer were manually trimmed using Staden Pregap (Laboratory
 30 of Molecular Biology, Medical Research Council, UK) running on a Sun Microsystem computer. Trimmed files were assembled into contigs using Staden Gap v4.1 and exported as FastA consensus files.

DNA sequence data was supplemented with sequence downloaded from the Internet site of the Institute for Genome Research
 35 (<http://www.tigr.org>).

DNA sequence analysis

DNA files in FastA format were converted to GCG format files before translation into amino acid files using the program Flip obtained from
 5 ANGIS (Australian Genomic Information Service, University of Sydney, Australia). FastA homology searching and/or PSORT analysis(4,6) were used as data mining tool to select potential vaccine candidates. All proteins with a PSORT probability of outer membrane >0.8 were selected. The FastA results for these proteins were then examined for any alignment with a
 10 protein suggesting surface location of vaccine efficacy.

All proteins were searched for homology against a non-redundant Bacterial protein database compiled by ANGIS using the FastA algorithm. The settings used for the FastA searches were Ktup = 2, gap creation penalty = -12, gap extension penalty = -2, width for deriving alignment in opt = 16
 15 and the Blosum 50 scoring matrix. Individual FastA search results were examined for significant homology by statistical probability and amino acid alignments.

The results are set out in Table 1.

Protein files were then trimmed to the first, second and third
 20 methionine residues using a protein trimming program (ANGIS). The trimmed proteins were then subjected to PSORT analysis (4, 6) for the detection of signal sequences and the prediction of protein cell location.

The results are set out in Table 2.

The sequences obtained are set out below. The relationship between
 25 these sequences is set out in Table 3. The initiation codon was calculated using a combination of sequence homology alignment (FastA), signal sequence prediction (PSORT) or ORF prediction (GeneMark) (3).

As will be understood by those skilled in the art open reading frames (ORFs) may be readily identified. ORFs may be determined using three
 30 methods, for example, alignments from FastA search results may be used to define the start and end positions of coding regions if sufficient protein homology is present. Alternatively, protein coding regions may be identified using the ORF identification program GeneMark (3) using a matrix trained on published *P. gingivalis* sequences. This matrix may be further refined by
 35 adding ORFs identified from the results of homology searching and ORFs identified by GeneMark. Otherwise, the program PSORT (4,6) may be used

for the detection of signal sequences at the start of a protein and the prediction of cell localisation. A UNIX version of TopPred (5) may also be used to identify potential membrane spanning domains.

5 It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this fourth day of August 1998

CSL LIMITED

Patent Attorneys for the Applicant:

F B RICE & CO

References.

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software for membrane protein structure predictions. *Comput. Appl. Biosci.*
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localization sites in Gram-negative bacteria. *Proteins: Structure, Function,
and Genetics* 11:95-110.

Table 1 Results of Fasta homology searching

SeqID#	Length of ORF in SeqID	Homology description	Length of homolog	% identity	Overlap (aa)	E value
45	589aa	Fimbrilin ORF3, <i>Porphyromonas gingivalis</i>	670	46	592	2.30E-99
46	907aa	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	578	23	572	7.90E-25
50	566aa	Outer membrane protein 11, <i>Helicobacter pylori</i>	186	25	183	2.00E+00
51	819aa	Ferric pseudobactin M114 receptor protein, <i>Pseudomonas</i> sp.	826	22	585	1.00E-05
58	973aa	Histidine kinase, <i>Pseudomonas putida</i>	978	28	554	4.80E-28
61	1162aa	Arginyl endopeptidase precursor, <i>Porphyromonas gingivalis</i>	991	24	328	7.30E-08
62	406aa	Outer membrane porin (porB), <i>Neisseria meningitidis</i>	332	23	239	4.50E-01
64	467aa	Component of alkaline protease secretion (aprF), <i>Pseudomonas aeruginosa</i>	481	21	427	3.40E-06
65	436aa	Outer membrane protein alkL, <i>Pseudomonas oleovorans</i>	230	26	136	2.70E+00
66	945aa	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	578	21	639	7.30E-09
71	563aa	Neuraminidase precursor (nanH), <i>Bacteroides fragilis</i>	544	23	251	1.50E+00
75	211aa	Attachment and invasion protein homolog (ail), <i>Salmonella typhimurium</i>	165	21	140	1.90E+00
77	953aa	Conserved hypothetical secreted protein (HP1216), <i>Helicobacter pylori</i>	660	20	483	4.10E-04
79	962aa	Protease I (API) gene, <i>Achromobacter lyticus</i>	653	24	695	1.80E-22
80	1312aa	Cysteine protease, <i>Porphyromonas gingivalis</i>	364-2628	25	212	0.00011
81	938aa	Cysteine protease hagD, <i>Porphyromonas gingivalis</i>	989-2628	31	742	1.40E-23

Table 1 Results of FastA homology searching

SeqID#	Length of ORF in SeqID	Homology description	Length of homolog	% identity	Overlap (aa)	E value
82	1251aa	Serum opacity factor, <i>Streptococcus pyogenes</i>	1025	24	176	2.10E-01
83	426aa	Vacuolating cytotoxin gene (vacA), <i>Helicobacter pylori</i>	160	32	111	1.60E+00
85	266aa	Outer membrane protein, <i>Neisseria gonorrhea</i>	174	22	153	6.60E+00
87	814aa	P1 cytoadherence protein, <i>Mycoplasma pneumoniae</i>	219	41	63	6.80E-01
88	451aa	TolC, <i>Salmonella enteritidis</i>	491	23	436	5.70E-11

Table 2 Results of protein analysis using Psort.

The type of signal sequence and the amino acid number of the most C-terminal residue of the signal sequence is listed. The abbreviations for cell location used in the table are: OM = outer membrane, IM = inner membrane, PS = periplasmic space.

The terminal amino acid may indicate surface location if it is an aromatic amino acid (F or Y).

* indicates an uncleavable signal sequence is present.

** indicates a lipoprotein signal sequence is present

Seq ID#	Signal present (Y/N)	Cleavage site	Cell location and probability			Terminal amino acid
			OM	IM	PS	
89	Y	20	0.94	0	0.31	N
90, 91	Y	20/24	0.82	0	0.19	F
92	Y	41	0.93	0	0.25	F
93, 94	Y	21/20	0.85	0	0.44	K
95	Y	28	0.93	0	0.25	F
96	Y	21	0.94	0	0.29	F
97	Y	32	0.93	0	0.26	G
98	Y	19	0.93	0	0.22	N
99	Y	27	0.94	0	0.32	H
100	Y	20	0.94	0	0.3	L
101	Y	21	0.93	0	0.24	F
102	Y	20	0.93	0	0.24	F
103	Y**	19	0.79	0.87	0	V
104	Y	24	0.94	0	0.32	L
60	Y	20	0.93	0	0.21	Q
105	Y	28	0.8	0	0.25	Q
106	Y	26	0.94	0	0.3	H
107	Y	20	0.93	0	0.19	F

Table 2 (cont.)

Seq ID#	Signal present (Y/N)	Cleavage site	Cell location and probability			Terminal amino acid
			OM	IM	PS	
108	Y	21*	0	0.18	0	F
109	Y	24	0.93	0	0.2	N
110	Y	57	0.93	0	0.21	S
111	Y	47	0.89	0	0.21	N
112	Y	22	0.94	0	0.32	V
113	Y	28	0.94	0	0.38	K
114	Y	18	0.93	0	0.25	F
115	Y	23	0.85	0	0.30	E
116	Y	25	0.88	0	0.35	N
117, 118	Y	19/18	0.89	0	0.25	P
119, 120	Y	25/23	0.93	0	0.25	N
121	Y	21	0.94	0	0.3	F
122	Y	19	0.85	0	0.3	R
123	Y	36	0.93	0	0.27	Y
124	Y	20	0.93	0	0.46	L
125	Y	20	0.86	0	0.25	Q
126	Y	21*	0	0.04	0	K
127, 128, 129	Y	24/20/21	0.53	0	0.2	P
130, 131	Y	25/24	0.91	0	0.31	Y
132	Y	29	0.93	0	0.21	F
133	Y	46	0.91	0	0.03	H
134	Y	24	0.93	0	0.24	F
135	Y	23	0.94	0	0.29	D
136	Y	25	0.85	0	0.37	R
137	Y	17	0.36	0	0.22	D

Table 3: Relationship between DNA and protein SeqID numbers

DNA sequence	ORF untrimmed	ORF trimmed to 1st Met	ORF trimmed to 2nd Met	ORF trimmed to 3rd Met
1	45			
2	46		89	
3	47	90	91	
4	48			92
5	49	93	94	
6	50	95		
7	51		96	
8	52	97		
9	53	98		
10	54	99		
11	55		100	
12	56	101		
13	57	102		
14	58	103		
15	59	104		
16	60			
17	61	105		
18	62	106		
19	63	107		
20	64	108		
21	65	109		
22	66	110		
23	67	111		
24	68	112		
25	69		113	
26	70	114		
27	71	115		
28	72		116	
29	73		117	118
30	74	119	120	
31	75	121		
32	76		122	
33	77	123		
34	78	124		
35	79	125		
36	80	126		
37	81	127	128	129
38	82	130	131	
39	83	132		
40	84	133		

Table 3 (cont.)

DNA sequence	ORF untrimmed	ORF trimmed to 1st Met	ORF trimmed to 2nd Met	ORF trimmed to 3rd Met
41	85	134		
42	86	135		
43	87	136		
44	88	137		

(2) INFORMATION FOR SEQ ID NO:1

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1768 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

20

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

25

agactatcaa atccatgaag gggcctatat cattccgggc aaagagcaaa tgcgaccact	60
attcaatggc aacaacaact tcagcatcta tgtagtggcc aatctcgatt tcaatgctcc	120
ggccacagaa gctgcgcttt ctcaatttgt ggtagagaaa tctattgaag tctcttctac	180
gacagcccct gccgatttcg taatgcttgc tcatggcaat aagcagatca atatggctac	240
30 gacagaaggg aaactgttgg gggattataa actcaaacga gtggcagcaa agattcgcat	300
gataaaaccc accatcaatg tgcaaggata tgaagtgggc ggaaatatac aggcaaagtt	360
tcgcaattcg gtaacgaagg ggttccttac cacagaagct caagagatcc cagctgctgc	420
atcctataag acatcggaat atcttgatat tgcagagtcg gcacctgcca attctatcca	480
tttctattct tactataaca aatggacact ctccacaccg gagaagcgac cggaattctt	540
35 catcatgggc aaattcaaaa agacaggaca gccggacaac acagccaaac cgtactacta	600
cagagtgccc ctcgaatctc aggacaatca ggtcaagagc aatgtcctct ataattctgaa	660

	tgtgaaaatc gaaatcttgg gttctttaca agagccggaa gctgtttctg taaacggcac	720
	actcgcaata gaagaatgga ttctccatca ggatgcattc aatctgcctg ccaccaatta	780
	cttgatagtg gaacagcacg aaatcttcat gaataacgtg aacacatact cggtgaaata	840
	tcaaacttcg cagaaaccaa tcagcattag catacagtca gttaccttta gctacgtctc	900
5	ttctgatggc actcagcaca atgatcttgt agcaagtagt agcgaccagt atcctacgat	960
	tacaagcgat aatacaagca tcataatcac ttccaagata ccggttaata acgtaccaa	1020
	gaagatcggt tttgaggtaa ctaatggggg agccggtttg aaagagactg tcacagtact	1080
	ccaatatcct gcacaattta ttgtcaatac acttggcaca gcatcggcat ggagaccaga	1140
	cggatctttg gctccggggc ttaacaataa agcgatttac catgtcgtag tactggttcc	1200
10	acccgagaat ttatttgaag atgggacaca gacaatcatc ggttatcccc cactgaaac	1260
	aatttctttt cataagaaag agaacaatac ctatccgata gtatggtctg acacaaatac	1320
	gacaaaacag gaccttgaga catcaagaat gatttcacct tcctttgagt tagcctccca	1380
	acttggggct actctcccga tgccttatct cgagtattgg ccaggacat catatctcct	1440
	tgactattcg ggaaactata ataataagag atacgccttg tttaattgcg ctttttactg	1500
15	ggagaaaaaga aaagttaata acgaagaaat taaattcgat gactggcggt tgccgacaga	1560
	agctgagatc aaattgatag ataagctgca acataatgag cagagtgtg tccaagctat	1620
	catgacaggg aattattatt gggatagtta ctctgcaaat gggctttata aaatgcaagg	1680
	aggagggggc caaggaaatt cctccaaagc ctatgttcgt tgcgtgcggg atgtgaaaaa	1740
	gccgattcgt gacaagaagt caggtaag	1768

20

(2) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 2721 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- 30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

5

(B) LOCATION 1...2721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

	ACTATATGCG TTGCCTTCTT ATCCGCTCCC GTTGCGGCAT TGC GCGAGTC GCCGCCAATG	60
10	GGGGCGGAGC GGAAGACTCC CTCTCTCCTA CCCCTTCTTT TCGAGCATTC TGATAAAGGA	120
	AAGGGGTTCG ACTACAGACT ATTCACAAGC AATAAACTTA AAGTGTTTGC CACAGGTAAC	180
	AGCCGATACA TACACAATAA ACCAACAATC ATCCAAGCAA TGAAACGAAT CGTTTTATCA	240
	TCTTTCTGT TCGTTCTGTC CATACTTTCT TTGATGGCAC AGAACAATAC CCTCGATGTA	300
	CACATATCCG GTACGATCAA GGATGCCTCC TCCGGCGAAC CAGTGCCCTA TGCCACTGTA	360
15	AGCATCCGGC TGACAGGAGC AGATACCACA CAGGTGTTCC GACAAGTGAC TGACGGCAAC	420
	GGCTACTTCG TCATAGGCCT GCCGGCAGCT CCCTCCTATC ACCTGACAGC TTCGTTTCGTA	480
	GGTATGAAAA CCCATACCAT GCAGATTAGT CGGGGAAATG GACAGCACGA CATCAAATCC	540
	ATCGACATTT CTCTCGAATC CGAGGACAAA CAACTCTCCA CCGTCACCGT ATCGGCAGCA	600
	CGACCACTGG TGAAGATGGA GATAGACCGC CTGTCTTATA ATATGAAAGA TGACCCCGCA	660
20	GCCAAGACGA ACAACCTGCT CGAAATGCTG CGCAACGTTT CTTTGTAAC GGTGGATGGT	720
	CAGGGCAATA TCCAGGTGAA AGGATCTTCC AACTTCAAAA TCCACCTCAA TGGCAGGCCC	780
	TCGACCATGG TGAGCAGCAA CCCGAAGGAG GTCTTTCGCT CCATTCCTGC CCATACGATC	840
	AAACGGGTGG AGGTCATCAC CGATCCGGGT GTAAAGTACG ATGCGGAAGG CACAAGTGCC	900
	ATCCTGGACA TCGTCACGGA AGAAGGTAAG AAGCTGGAAG GATATTCAGG TTCCATCACG	960
25	GCCAGTGTCA GCAACAATCC CACAGCCAAC GGTAGTATCT TTCTGACGGC AAAGTCCGGC	1020
	AAAGTCGGGC TGA CTACCAA CTATAACTAC TACGGTGGCA AAAACAAGGG CTCTCGCTAC	1080
	TTTACCGAAC GTACTACATC CATGCTCCAA ACGATAGAAG AAGGCAAAGG GCAAGAAACC	1140
	TTTGGCGGAC ACTTCGGCAA TGCCCTCCTC TCATTCGAGA TAGATTCGCT CAATCTCTTT	1200
	ACGGTGGGCG GCAATGTACG CCTTTGGGAG ATGACCACCG ACCGGAACAG CGTAGAAAAA	1260
30	AGCTTTGCCG GCAGCAACCT CATGTCCTAC ATAGACAGAA AACTCAAAAC ACAGATGGAT	1320
	GCCGGATCAT ACGAGCTCAA TGCCGACTAT CAGCACAGCA CTCGCCTGCC GGGCGAATTG	1380
	CTCACCGTTT CCTACCGCTT CACTCACAAT CCTAATAATA GCGAGACCTT CATTGACCAA	1440
	TGGAAGCGCG ATCCGCTCAA CACAGCTAAT ACGATCCAGT ACGCCGGCCA GCACTCCAAA	1500
	TCCGATGCGG GCATGGACGA ACATACGGCA CAAGTGGACT ATACACGTCC CTTAGGACAA	1560
35	GCACATTCTT TGGAAGCAGG GCTGAAGTAC ATCTATCGTC ATGCCACGAG CGATCCTCTC	1620
	TATGAGATAC GACCATCCGA AGATGCTCCG TGGCAGCCCC GCTCTCTATA TGCACAGAAT	1680

CCGTCGAACG GAAAGTTCCG CCACGATCAA TACATCGGAG CAGCCTATGC CGGCTACAAC 1740
 TATCGTAAGG ATCAGTATTC TTTGCAAACC GGCCTCCGAG TGGAAAGCAG CAGGCTGAAA 1800
 GCACTCTTTC CCGAAAACGC AGCAGCAGAT TTCTCCCACA ACTCGTTCGA CTGGGTGCCA 1860
 CAGCTCACGC TCGGCTATAC CCCCTCGCCC ATGAAGCAGC TTAAGCTGGC CTATAACTTC 1920
 5 CGAATCCAAC GTCCTGCAAT CGGCCAACTG AATCCCTACC GGCTACAGAC CAACGATNAT 1980
 CAAGTACAGT ATGGTAATCC CGACCTAAAG TCGGAGAAGC GTCACCACGT CGGTCTCTCC 2040
 TATAATCAAT ACGGAGCCAA GGTCATGCTT ACAGCATCGC TCGACTACGA CTTCTGCAAC 2100
 AACGCCATCC AGAATTACAC CTTCTCCGAC CCGGCCAATC CCAATCTGTT CCACCAGACC 2160
 TATGGCAATA TCGGACGAGA GCATTCTTTC AGCTTGAATA CCTATGCCAT GTACACGCCG 2220
 10 GCCGTATGGG TCAGGATTAT GCTCAACGGA AATATCGATC GCACATTCCA AAAGAGCGAA 2280
 GCACTCGGCA TTGATGTCAA TTCATGGTCC GGCATGGTAT ACTCAGGCCT GATGTTCCACC 2340
 CTGCCGAAGG ATTGGACTGT GAATCTCTTC GGAGGTATT ATCATGGGGG AAGAAGCTAC 2400
 CAGACGAAGT ATGATGGCAA TGTATTCAAC AATATCGGTA TAGCCAAACA GCTTTTCGAC 2460
 AAAAAATTGA GAGTCTCGCT GAGCGCAAAC AACATTCATG CGAAGTATTC GACATGGAAG 2520
 15 AGCCGGACCA TCGGCAATGG ATTTACTATT TATTCGGAAA ATGCCGGTAT ACAACGGAGT 2580
 GTTTCCTCA GCCTCACCTA CAGCTTCGGT AAGATGAATA CACAAGTGCG CAAGGTAGAG 2640
 CGTACGATCG TCAACGACGA CCTCAAGCAA ACCTCATCCC AAGGACAGCA GGGTGGCGGA 2700
 CAAGGAAATC CTACCGGCAA T 2721

20

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1818

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

	ATAATCTTCT GTACGATTCA TCACTCTGAG TTGGAAATAA TGAACAGCAT CATGAAATAT	60
	CAATTATATA CGGCCGTCAT AATGGCTCTC TCTGTATCAT CCGTTTGCGG TCAAACCCCA	120
10	CGAAATACAG AAACCAAACG CCCCAGACACG CTGCGCAGGG AGCTTACTAT CGTTAATGAC	180
	CAGACTGTGG AGATGGAGCA TGC GGATCCG CTTCCGGCTG CATAACAAGGC CATCGAACCT	240
	CGATTAAAC CTTTCCGTCC GGAATATAAC AAGCGTACAT TCGGATTTGT CCCTGAAGTT	300
	TCCTCTTCAG GCAGGAACAA TCTTCCGAAT ATCCTGCCGA CGGAAGGTCA TATGAAGCAC	360
	CGGGGGTACC TGAATATCGG TATCGGCCAT ACGCTAAACC AGCGAATGGA TGCCGGCTAT	420
15	CGTCTGATAG ATGCAGAGCA GGAGAGACTG AATCTTTTCC TCTCCTATCG TGGGATGAAA	480
	TCGGCTTTCA ATACCGGTGA CTTGACGGC GACAGAAAGG ATAGACGAAT GATGGCAGGA	540
	GTGGACTACG AGCAGCGCAG GCCTTCCTTT GTGCTTGCTA CCGGCTTGTA TTATTCGAAC	600
	CATTATTTCA ATAAC TACGG ACGGGGAGCT ACCACCAATG TGGGCAGCAT CCCTCAGCTA	660
	TCGACACCTG TTA CTCTCA GATGGACAAC GGGACCCACA ACGTCCGTGT ATACTTGGGT	720
20	GCAAAAAATG ATGTGATCGA TGCCAGGATC GACTATCGTT TCTTCCGTTC TATTCCCTAT	780
	CTGGGTACCG ATCCGATGAA GGCTCTCACA GAACATACGC CTGAACTGAA CGTGACGATG	840
	AGTAATGAGT TGTCCGATGA TATTAAGCTC GGTGTGGAAG TTCGTACGGG AGGATTGTTT	900
	TTTGCCAAAA ACAGCGAAAT GATTCAAACG GCGTTCCTGT CCGAAACCGA CCGCAACCTG	960
	TATTATGTGG AGGGCGCGCC CACAATCGGA TTTGTGCGAG ACTCGGACAA- TATGCAATGG	1020
25	AACATACAGG CCGGAGTAGG GATTTCTTCC CATTTGCGAG CCAAAGGGAG GTTGTTTTTTC	1080
	TGGCCTAAAC TGGATGCTTC GCTTAGTATC TTCCCTTCAT GCGTGTGTA TGCGAAAGCC	1140
	TTCGGCGGTG TGATTCGAAA TGGTCTCGCC GATGTTATGC AAGAGGAGAT GCCCTACCTG	1200
	ATGCCCAATA CGATTGTACT CCCTTCGCGC AATGCTTTGA CCGCCCAATT AGGGGTGAAG	1260
	GGGAATATAG CCGATGTGGT ACGTATGGAG GTTTATGGCG ACTTCTCCAA GCTGACAGGT	1320
30	GTGCCTTTCT ATACTCCGAC TCTACCCTTA TATAATCCAT CCGACTTGTA TCAGTATAAT	1380
	GTGAGTTTCT TGCCGATATA TGCCGACGGC AGCCGCTGGC GCGCAGGTGG TAAGCTGGAA	1440
	TACTCTTATC GCGATATGCT CCGCTTTCTG GTAGACGCAT CCTATGGCAA GTGGAATTTG	1500
	GATGGAGGAC TTGTGCCTC CATGCAGCCC GATCTTATAT TGAAGGCAGA AGTAGGTGTT	1560
	CATCCCATTG CCCATTGGA TGTCAGACTC CCGTATACAC AGCTGAACGG ACGGTATCGG	1620
35	TATTCTTTTCG GCTCGGCTGG CTCGGAAGCC TTGGGTATCG GTAATGTACA TCTTCTTAGT	1680
	GCGGATGTTT CATACAAGCT GAAAAAGAAC TTGAGCCTTT ATCTCAAAAT CGATAATATG	1740

CTGGCGGAAA CGACAGAGCT TATCGGTTAT TATCCTATGC AGCCGTTCCA TTGTTTCGCC 1800
GGTTTTAGCT GGA CTTTC 1818

5 (2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1071

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

AACTCCCATG CAACAGTCTC CGTTATATGT TCAATGATGG AAAAATGTAT CTTTGCTCAC 60
TATCCACATA ACCTTGTTGTT CATGATTCGC AAGCATTTTCG GTATCATTTT GGGATTTCTT 120
30 TCTCTTGTGT TTTCGGCAGG TGCTCAACAA GAGAAGCAGG TGTTTCATTT TCTGAACCTT 180
CCGGCTACTG CACAGGCTTT GGCTGCCGGA GGCAAAGCTA TCACCATCGT AGACGACAAT 240
CCCGGACTGG CTTTTGAGAA TCCGGCTCTG CTCGGATATG AATCCGGTGG CCGCGCCTTT 300
CTTTCCTATT TATATTATAT GAGTGGTTTCG CATATGGGCA ATGCCTGTTA TGCCTCGTCC 360
GTCGGAGAGC GTGGCATGTG GGGTGTGGC ATGCGTTTCC TGAACACGG GTCTATGCAA 420
35 GGATACGATC AGAATGCGAT TGCCACCGGC TCTTTTAGTG CTTCCGATAT AGCTGTACAA 480
GGATTTTACA GCCATGAACT GAGCAACCAC TTCCGCGGTG GAGTCAGCCT AAAAGCATTG 540

TATTCTTCTA TCGAGACGTA TAGTTCCTTT GGCCTTGGTG TGGATGTCGG TATCAGTTAT 600
 TACGACGATG ACAAAGGATA TTCCGCTTCC GCTCTGTTCA AGAACGTAGG GGCGCAACTG 660
 AAAGGCTATA ATGAAGAACG GGAACCGCTC GATTGGGATT TCCAGCTCGG CTTTTCCCGC 720
 AGTTTTATCA ATGCTCCGTT TCGCTTGACAC ATCACGTTGT TCAATCTGAA TCCGCACTAT 780
 5 TTCAAGCGTC TTGTACCACG CGATCTGTCC AAGATGCAAA AGTTCCTCCG ACACTTCTCG 840
 ATAGGAGCAG AATTTACTCC TTCCGAGAGG TTTTGGGTCG GGCTGGGATA TACGCCACAG 900
 ATTGCACAGG ATTTGAGAGT GGAAGGCGGC AACAAATGGG GAGGTCTTTC GGCCGGCGTC 960
 GGTTCACACTT CAGGTGTAGT ACGTGTAGGC GTATCTGCTG CCACCTATCA TCCTGCAGCT 1020
 CTTTCGTTCA TGTGTTCCGT AGGTATCCGT TTGGACGATA AGAGCATCTT C 1071

10

(2) INFORMATION FOR SEQ ID NO:5

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 30 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

35 AAGTTTATGA TGAAAAAGC ATTTGTTTTT GTACTACTGG TTTGCCTATT CTCCTCGTTC 60
 AGCAGTTCCG CCCAAACAAC GACGAACAGT AGCCGGAGTT ATTTTACAGG ACGAATCGAG 120

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AAGGTGAGTT TGAACCTAGG GGTCCCCCCC GTAAGCACAG AGGTTTGGGG AATGACCCAT      180
GATGCGAACG GTCTCCCTTT CGAAATACCT ATCTCTTTCA GTCGTTTCAA CAGCCAGGGA      240
GATATAGCTA CCACTTATTA CATAGCGAAT AGCGAGGCAA CTTTGAATGA ATGGTGCGAC      300
TATGCACACC CGGGCGGCAT CGTGAGGGTA GAAGGTCGTT TTTGGAAAAT GACTTACAAC      360
5  ATACCAACCT ACAATGCAGT CTGCACCCGG ATTACATTCG AAAATCAAGA AATAGAAGGA      420
ACGATCGTCT TGATACCCAA GCCCAAAGTC TCGCTGCCTC ATGTGTCGGA ATCGGTGCCT      480
TGCATCCGAA CCGAAGCCGG GAGGGAATTT ATCCTTTGCG AAGAAGACGA CACCTTTGTG      540
TCTCACGATG GTAACGAAGT AACGATAGGC GGTAAACCTT TCTTGCTCAA TACCAACGTA      600
AAGATTGTGG GGGACGTATC TCAAAAGTAT GCCGTGGGGG TAGGAGAAAT TCGATTCTCTG      660
10 CAGATTTGTG CCCAAACAGT ATCACAACAA AAA                                     693

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(2) INFORMATION FOR SEQ ID NO:6

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15      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1698 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: circular
20
      (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: NO

25      (iv) ANTI-SENSE: NO

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis

30      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...1698

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6
35
TACGACGGAG CGAGACTGGT CTATACCCTA TTTCGGAATA GAAACGACAT TCACCCTATG      60

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AAAACCAT TG TAAGATACAG CCGCCTTCCG GTCGCTCTCT TCTTTTGCCT TTTGGGAGCT 120
 GTGCACTTGT CTGTCGAGGC GCAGATGCTC AATACTCCTT TCGAGCTGTC GGATCAGATC 180
 GTCCTGTCTC CCACCGAAAG GCAATACAGG GAGATTTGTG TGCAAACGAA AGAAAAAAGG 240
 GGGGCCGATC TTTTCCCGTT GAGCGATAAG CTGCGCGATT CGGCCTATGT TCGTTTCGGC 300
 5 TCGGCCTATG GCGATATTGC GGGCGACTAT CTTCCGTACA ACGGCAATAA CTACTCCTCG 360
 CTCTCGCTCG AATCGGGTGG TCGCATCAGT GTCCGTA ACT ATGGCACATT GCAGGGCAGT 420
 GCTTCCTACT CACGTGGCAT GCACAAACGC ATCGGCTGGA ATGCTCTGCG CAACGCCGAA 480
 GCCTACTATC CCTATTTGGT GTCCGATTCG ACCGGCGGAG ACTATCATTT CGAAGACTAT 540
 CGGCTTGCCG GCTACTATTC TTTTCGCGCC GGCCGCTTGC CCCTCGGTAT AGGCTTCTCA 600
 10 TACAGGGGCG AAGTTGCTTA TCGGCTGACC GATCCGCGTA CGACCAATAC GACCGGTGCA 660
 TTGGAGCTTT CTTGTGCTAC CTCTTTGACG CTGCCTCGAG AGAACAGGCT ATCGCTTTCG 720
 GCTGCGTATC TCTATCATAG ACAACACCTC ACACAGTACA ACTGGCGTCC CGGGCAGCAG 780
 GACAAATTCT TCGTCAGCTA CGGTTTCGGT CAGGTGGATG TCAGCAACAG CCCTATCTGG 840
 TTCGGTATCT CCAGAATGAA CTACGTCAAC GGATGGAAGC TTAGCTCCCG TCTGGATACC 900
 15 CGTAGGGGCG ATGCCATCGG TCTCGACTAC AGCGGCTACT TCCTCGATAC CGAaGAGAGG 960
 TCGTCCATCA ATCTCTTTGC TTTGCTTTAC AATCGCCTGC GACTCTATGG TAGCTGGCAT 1020
 CTGTCCGACT TCGATTTTTT CTTTTTCAGCC GACTATGCTC TCGCCAAGG GATAGAGCGG 1080
 ATATACGAAG ACTACAAGCC GGATGATAAT TATCATATCT ACGACCTCCG TATCTTGGCC 1140
 ATTCGCCGCT GGTATATGCT CAATGAGTTT TCTGCCCAAG CCCAAGCCTC CTACCGTATT 1200
 20 CGCACGGATA GAGGTTGTGC CCTGAGAGTG AGTGCCGGTA GTGATTTCTA CGGCTATGAT 1260
 GAGACGTATC GCAAGCATGG ACATCATACC ATGAGCGGAA TGCTACGTCC TTTTGCCGGT 1320
 ATAGCCTATG ACCATGCCGG ATCCAAATTG GATTTTGGAC TTTCGCTTTC GGCTGCTTAT 1380
 CGAATGGTGC TGACGCATTC GTATAAGATT CGTACCATCC AGAAAGAGCA GCTCGACTAT 1440
 CAGCTGGCCT ATTTGCCCTA TGCCTATCGT AATAGAGAAAG GCGTGGAGGT GCGTTCCTCT 1500
 25 CTGTACGTCT CGATTCCGAT GCAGAATACC CACCGCTGA TGACAGAGCT GCGGTTGTAT 1560
 GGCGACCTGA TGAAAAGAAA GGACGGTATA GCCTATGGCA AAACGCCCCG TGTCATCTCA 1620
 CATATCCTGT CCGATCCGCA AGCCGAACGA ACGTCCGGCC ATACCATCGG GGCTATCTGC 1680
 AATATCTCCT ACCTCTTC 1698

30

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2457 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2457

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

	AGGACGAACG TTTTCTTATC TTTGTCCCAT AAAATTGGGA GAAGGGGTGC TTCCTGTAGC	60
	AATCGGAATG CGTGGATGGC TGAGAACAAA CCCTCATCAC CTGAACCGGA TAATACCGGC	120
20	GTAGGAAACT CTCCGTCTGA CTATCTTCAC GGCGAAGCAA TCATTCCCCC TCTCTCTTCT	180
	TTGTCCAACT TCAATGATAA GAGATTTATG AAAAACTTC ACATGATTGC CGCCTTAGCC	240
	GTCCTGCCTT TCTGCCTGAC GGCACAAGCA CCCGTCTCCA ACAGCGAGAT AGATAGTCTT	300
	AGCAATGTGC AGCTCCAGAC CGTACAGGTC GTAGCTACTC GCGCCACGGC GAAAACCCCT	360
	GTCGCTTACA CCAACGTTCG CAAGGCCGAA CTTTCCAAGT CCAATTATGG TCGTGACATC	420
25	CCCTATCTGC TGATGCTGAC TCCCTCCGTG GTAGCCACCA GCGATGCCGG TACGGGTATC	480
	GGATATTCCG GCTTTCGCGT GCGTGGCACC GATGCCAATC GCATCAACAT AACTACCAAT	540
	GGAGTACCCC TCAACGACTC CGAATCTCAG TCCGTCTTTT GGGTGAATAT GCCCGACTTC	600
	GCCTCTTCCA TCGAAGACCT TCAGGTGCAG CGAGGTGTGG GTACTTCCAC CAATGGTGCC	660
	GGAGCTTTTG GGGCAAGTGT CAATATGCGT ACGGATAATT TGGGACTGGC TCCTTATGGC	720
30	CGTGTGATT TGAGCGGAGG TTCGTTCGGC ACATTCCGCC GATCGGTCAA ACTCGGTAGC	780
	GGACGCATCG GTCGCCATTG GGCAGTGGAT GCCCGCCTGT CCAAAATCGG TTCGGACGGC	840
	TACGTGGATA GAGGAAGCGT GGATCTGAAA TCCTATTTTCG CACAGGTGGG CTATTTTCGGT	900
	AGCAACACGG CTCTCAGGTT CATCACTTTC GGAGGAAAAG AAGTTACGGG TATCGCATGG	960
	AACGGTCTTT CCAAGGAGGA TGAAGCCAAA TATGGCCGCC GATACAACAG TGCCGGTCTT	1020
35	ATGTACGTGG ACGCGCAAGG AGTACCGCAC TACTACCACA ATACCGACAA TTACGAGCAG	1080
	CGTCACTACC ATGCCATCAT GACGCACAGC TTCTCTCCTT CCGTTATCCT CAACCTCACG	1140

	GCACACTACA	CGGCCGGATA	TGGCTATACG	GACGAATATC	GTACCGGACG	TAAACTAAAG	1200
	GAATATGCAC	TGCAGCCCTA	TGTGGAAAAC	AGTGTGACCG	TGAAGAAAAC	GGATCTCATC	1260
	CGTCAGAAGT	ATCTGGACAA	TGACTTCGGA	GGACTCATCG	GTTCGCTTAA	CTGGCACACC	1320
	GGTGCATGGG	ATTTGCAGTT	CGGGGCCTCG	GGCAATATCT	ATAAAGGAGA	CCACTTCGGC	1380
5	CGTATCACTT	ACATCAAAAA	GTACAATCAG	CCCTTAGCTC	CCGACTTCGA	ATATTATCGG	1440
	AACAGGGCAG	ACAAAAGAGA	AGGTGCAGCC	TTTGCCAAAG	CCAACTGGCA	GATCACTCCG	1500
	GAACTGAACA	TGTATGCCGA	CCTCCAGTAT	CGTACCATCG	GCTACACGAT	AAACGGCATC	1560
	ACGGACGAAT	ATGATGAGGT	ACAGGGAAGT	ATGCAGCACA	TCGATTTGGA	CAAGACCTTC	1620
	CGCTTCCTCA	ATCCGAAGGC	CGGTCTTACC	TATAGTTTCG	ACGATGCTCA	TACTGCCTAT	1680
10	GCTTCTGTTG	CGGTAGCACA	CCGCGAGCCT	AACAGAACCA	ATTACACCGA	AGCCGGAATA	1740
	GGACAGTATC	CTACGCCTGA	GCGACTGATC	GACTATGAGC	TGGGCTACCG	CTATGCTTCG	1800
	CCCCTCTTGT	CGGCCGGAGT	AGGTCTCTAT	TATATGCAAT	ACAAGGACCA	ACTCGTGCTG	1860
	GATGGCCGTT	TGAGCGATGT	GGGACAGATG	CTCACAAGCA	ACGTCCCCGA	CAGCTACCGT	1920
	ATGGGACTGG	AGCTGACTCT	CGGTGGCGAG	ATCCTTCCTC	GTTTGCTGCG	TTGGGATGCT	1980
15	TCTTTCACTA	TGAGTCGCAA	CAAAATCGAC	CGCTACGTAC	AATATACATC	CGTATATGAT	2040
	GCGGACTACA	ACTGGCTCGA	ACTCAAGGAG	GAGACCCTCG	AAAGCACGGA	TATAGCCTAC	2100
	TCGCCCCAATG	TCATTGCCGG	CAGCATGCTT	ACCCTCTCTC	ATGCCGGTTT	CGAAATGGCT	2160
	TGGACGAGCC	GCTTCGTCAG	CAAGCAATAT	CTGGACAATA	CACAGCGCAG	CGATCGCATG	2220
	CTTTCCTCCT	ATTGGGTGAA	CGACCTCCGC	CTCGGCTATG	TGCTGCCGGT	TCACTTCGTT	2280
20	AAGAGAGTGG	CACTGGGCGT	ACAGCTCAAT	AATCTCTTCA	ACCTCATGTA	TGCGTCCAAT	2340
	GCCTACATCT	ACGATGCCGG	TTACGTACAG	GCATCCGGAG	AACTAAGTGC	ATATGCCGAT	2400
	CTGCGTTATT	ATCCTCAGGC	CGGATTTAAT	GCACTGGGTA	NTCTGACAAT	CGATTTC	2457

25 (2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 957 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

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(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...957

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

	TTTACGTCCG GTACGATATT CGTCCGTATA GCCATATCCG GCCGTGTAGT GTGCCGTGAG	60
	GTTGAGGATA ACGGAAGGAG AGAAGCTGTG CGTCATGATG GCATGGTAGT GACGCTGCTC	120
	GTAATTGTCG GTATTGTGGT AGTAGTGCGG TACTCCTTGC GCGTCCACGT ACATAAGACC	180
15	GGCACTGTTG TATCGGCGGC CATATTTGGC TTCATCCTCC TTGGAAAGAC CGTTCCATGC	240
	GATACCCGTA ACTTCTTTTC CTCCGAAAGT GATGAACCTG AGAGCCGTGT TGCTACCGAA	300
	ATAGCCCACC TGTGCGAAAT AGGATTTTCAG ATCCACGCTT CCTCTATCCA CGTAGCCGTC	360
	CGAACCGATT TTGGACAGGC GGGCATCCAC TGCCCAATGG CGACCGATGC GTCCGCTACC	420
	GAGTTTGACC GATCGGCGGA ATGTGCCGAA CGAACCTCCG CTCAAATCGA CACGGCCATA	480
20	AGGAGCCAGT CCCAAATTAT CCGTACGCAT ATTGACACTT GCCCCAAAAG CTCCGGCACC	540
	ATTGGTGGA GTACCCACAC CTCGCTGCAC CTGAAGGTCT TCGATGGAAG AGGCGAAGTC	600
	GGGCATATTC ACCCAAAGA CGGACTGAGA TTCGGAGTCG TTGAGGGGTA CTCCATTGGT	660
	AGTTATGTTG ATGCGATTGG CATCGGTGCC ACGCACGCGA AAGCCGGAAT ATCCGATACC	720
	CGTACCGGCA TCGCTGGTGG CTACCACGGA GGGAGTCAGC ATCAGCAGAT-AGGGGATGTC	780
25	ACGACCATAA TTGGACTTGG AAAGTTCGGC CTTGCGAACG TTGGTGTAAG CGACAGGGGT	840
	TTTCGCCGTG GCGCGAGTAG CTACGACCTG TACGGTCTGG AGCTGCACAT TGCTAAGACT	900
	ATCTATCTCG CTGTTGGAGA CGGGTGCTTG TGCCGTCAGG CAGAAAGGCA GGACGGC	957

30

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

10

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...729

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

	TCGACAATAA TGAAAAAAGC TATTCTTTCC GGAGCGGCCT TGCTCCTCGG CCTATGTGCC	60
	AACGCACAAA ACGTGCAGTT GCACTACGAT TTCGGTCATT CCATCTACGA CGAACTAGAT	120
	GGACGTCCCA AACTGACTAC CACAGTGGAA AACTTCACAC CCGACAAATG GGGGAAGCACC	180
20	TTCTTCTTCA TCGACATGGA TTACACGGGC AAGGGTATCC AGTCGGCCTA TTGGGAGATT	240
	TCGCGCGAAC TGAAGTTTGT GCAAGCTCCC GTTCCATTC ATTTGGAGTA CAACGGAGGC	300
	CTCTCCACAA GCTTTACTTT CGGACACGAT GCTCTAATCG GTGCCACCTA CACCTACAAC	360
	AACCCCTCCT TTACACGTGG ATTTACGATC ACGCCCATGT ACAAGCATCT GGGTGCGCAC	420
	GACTTCCACA CCTATCAGAT CACCGGCACT TGGTACATGC ACTTTCTGGA CGGTCTGCTT	480
25	ACCTTCAACG GCTTCCTCGA TCTTTGGGGT TTCCCCCAAG AGAACCCAAT CGGGGGCCCT	540
	GTGCTCAAAG AAGGGGATAA GTTCGTATTC CTGTCCGAAC CGCAGTTCTG GATCAACCTC	600
	AATCGCATCA AAGGCATCGA CAAGGATTTT AATCTCAGCA TAGGGACAGA GATGGAAATC	660
	AGCAGGAACT TCGCTCGCAT GGACAAATTC TCCTGCATCC CTACTCTTGC GGTCAAATGG	720
	ACTTTCAAC	729

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(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 1350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15 (B) LOCATION 1...1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

	TGGTGCCAAT CCGACCCAAT ACCTCATTGC CATGCAGTAT ATCGAAACGC TCAAGGACAT	60
20	CAACAAGGGC GATCAGACCA AGACCGTTTA CCTCCCGTTC GAGGCTACCG GTATGCTCGG	120
	TGCCTTGGGC GGTATGAAGG ATTTGGTGAA AGGATGAGAC TCTCTGCCAT TCTTATCGCT	180
	TTGATTGTGA TGCTGCCTGC TGTGCTTAGC GGGCAGCATT ATTATTCCAT GGCGGGAGAG	240
	CGACTGGAGA CGGACAGCAT TCGTCCGAAC GAACTCTCGG CATCGATCCG AAGTGCCTT	300
	TTCTTTTCGGA ACAATGAATA CAATGCACGT TCGGTCAAAG GTTATACGTT GCCGGGTGCA	360
25	CGGGTTTCCG CTTTTGCCTC TTA CTGCTG CCGGCAGCAC ATGGTGTGAA GCTTTCGCTC	420
	GGAGTATCTA CCCTGAACTA CTGGGGGGCA AGTCGCTATC CGGCCGGTAT CGCTTATTCC	480
	GATTTACCTT ATTGGACGGA CTATAACGAC TATGTACGCT TGCGTATCCT GCCTTATGTA	540
	CAGGCCATGC TGAAGCCGAC GGCCACGACT GCTCTCATGC TGGGCAATAT AGCCGGTGGT	600
	ACGGCTCACG GACTGATCGA ACCGATCTAC AATCCTGAGT TGGATTTGAC GGCTGATCCT	660
30	GAAGCCGGTG TGCAATTTCG GGGTGATTGG ACACGTTTCC GAATGGATGT TTGGGTCAAT	720
	TGGATGAGCA TGATTTTCAA AAATGACAAT CATCAGGAGT CGTTTGTCTT TGCTTGTCC	780
	ACTACTTCGA AATTGTTATC GGGTGAAGGC AAATGGCGAC TCGAACTGCC CTTGCAGGCT	840
	ATTGCCACGC ATCGCGGCGG GGAATACAAC TGGGCGCAGC AGGATACCGT GCATACATGG	900
	GTCAATGGAG CTGTGCGACT TAAGCTTTCG TATCGCCCTC GTACCGACAA ACCCATGCAG	960
35	ATTTGGGGAT CTGCTTATGG TGTGGCAGCC TTGTCAAGCG GAGGATACTT CCCTTACGAA	1020
	AGAGGGTGGG GCGGTTATCT TTCTCTCGGA ATGGACTTGG AGCACTTCGC TTTTCGTACC	1080

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GACTATTGGT ACGGCAGGCA TTACGTTTCT CCCTTTGCTG CACCTTTCGC CAATTCCCTG 1140
ACGTATGACA AACAGCCTCT TACGAACGGT TGGGGCGATT ATATTCGTCT CTATGCCGAC 1200
TATTCGTGGC GGATGGCACG AAGTGTTTCG TTGGCGGCTG TTGCTCGGGT ATGGTTCCAG 1260
CCTTCGGATC GTTTTGCGAT GAGCCACGCC TTGGAAGTGA CGATGCGTAT CGATCCCCAA 1320
5 TTCCAATAG CTTTCTGAA AGGCAATCAT 1350

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(2) INFORMATION FOR SEQ ID NO:11

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10      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1341 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: circular

15      (ii) MOLECULE TYPE: DNA (genomic)

          (iii) HYPOTHETICAL: NO

20      (iv) ANTI-SENSE: NO

          (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis

25      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...1341

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

30      CCGTTTTTAC CGCCATGGGT ATGTGCTGGA GCGGCTTCCT CAGTACGCAC ACGGCCATGC 60
          TCGACAGTCT CAAGTACCGC CGCCTCATCA CACAGGCGAT CGGAGCACAT GCGATCGGCG 120
          GACTCGTCGC CGGCATATTC GCCCATTTGGC TCTTTGTCCT CATCTCACTC ATTTGATTCTG 180
          ATACCCGACC AACGTATGAA CAAATCGCTA TTATCATTTGG CATGCCTCAT CCTGTGCGGT 240
35      ATGCCGGCCA TCGCCCAACA GACAGGACCG GCCGAACGCA GCGGCGAGCC TTCTCTGGCC 300
          GAACGTGTAT TCGGTCTGGA GCAGAAGCAG AAAAAGCTGA AGGTGTACTT AGGCATACAG 360

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TCGTTCTACG ACCAGCCGCT TGTCGATGAC GAATCCCATATA TCGGACACTT CAAGGTACAG 420
 GAGCTGCGGA TGTCTGCTCA TGGCGAACTG AACCGCCACC TCAGCTTCGA CTGGCGACAA 480
 CGTCTCAACC GTGCCGCCGA CGGCACTTCG TTTGCCGACA ATCTCTCCAA TGCCATCGAC 540
 ATCGCAGGTG TGGACTGGCA CCCGAACGAC AAGGTGTCTT TCTTCTTCGG ACGTCAGTAC 600
 5 GCGCGTTTCG GAGGGATAGA ATACGACATG AACCCCGTAG AGATCTACCA GTACAGCGAC 660
 CTTGTGGATT ACATGACCTG CTATACTTCG GCGTGAACT TCGCATGGAA CTTCCACCCC 720
 GAACAGCAGC TGCAGCTACA GGTACTCAAT GCTTACAACA ACCGCTTCGC CGACCGCTAC 780
 CACGTGACAC CCGATGTCGC TACCGCCACG AGCTACCCGC TCCTCTACTC GGCACAGTGG 840
 AACGGTACCC TCCTCGGAGG AGCACTGCAT ATGCGTTACG CCGTGTCGAT GGCTCATCAG 900
 10 GCCCAAGAGC GTAATATGTG GTACTTCACT GCGGGCAACC TGTTCATCC GGGCAAACGG 960
 ATCAACGGAT ACCTCGACCT CACCTACTCG ATCGAGGGAT TGGACGACAA AGGCATTATG 1020
 ACTGCTCGCT ACGGCAAGGG CAAGACCCTC ACGGACGTCA AGTACTATGC TCTGGTATCG 1080
 AAGTGGAAC TCCGCATTTT CGATCAGGTC AATCTCTTCC TCAAAGGCAT GTACGAGAAC 1140
 GGCTATGCGC CTGCCCAATA CGGCGAGAGC AGCCACACGC GCCACTCCTA CGGCTATATG 1200
 15 GGAGGGGTGG AATATTACCC TACGGAGACC AACTTCCGTC TGTTTCGTAC CTACATAGGA 1260
 CGGCATTACC GGTACAGTGC GACCGAGACG GAAAGCACCA ATGCTCTTCG CGCCGGTCTG 1320
 ATCTATCAGA TACCTTTCTT A 1341

20 (2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1596

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

	TACAGGCGAT CGGGAAGGGT TTGTCTCGT ATCCTCCGGA ACAAACGTTC CTACGCAGAT	60
	ACTCGGTTAC AGCCGAGAAG AGCGGTTCTGA CTACGAGCCG GCACCAGAAC AAAGATGAAA	120
	AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCATCAGCCT TTCTGCTCAG	180
10	CGGTTTCCGA TGGTGCAGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TCTGCCCAAG	240
	CGTCCTTGGC GCGCCATCGG TAAACGATA GCGTCAATC TGGCCGTATG GGGCTTCGAT	300
	CATTTTCATCA TGAACGAGGA CTTTGACAGAC ATCAGTTGGC AGACTATCAA GAGCAATTTT	360
	CAAACAGGCT TTGGCTGGGA CAATGACAAG TTTGTACCA ACCTCTTCGC ACATCCTTAT	420
	CACGGATCGC TCTATTTCAA TGCAGCGAGG TCGAACGGTT TGAGCTTCAG GCACTCTGCT	480
15	CCGTTTGCCT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCGAGT	540
	ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG	600
	CTGTCCGACC TGCTCATCGA CAATCGTACC ACAGGGTGGG AACGTATGGG GCGCGAGGTG	660
	GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT	720
	TCTGTCCGGA GTCGCAGCGG ACAGATATTT CAGTCTGTCC CCATAAACAT AGTCGTCGAT	780
20	GCCGGCTTTC GCTTTTTGGC AGACAAGCGG CATGCCCCGAA CCGGTGCCAC GGCTCTGACC	840
	CTGAATCTGA GATTCGACTA CGGCGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT	900
	TTCTTCCAAT TCAAAGCCGG ATTGAGTTTC TCCGAATCGC AACCTCTGCT GAGCCAGATC	960
	AATCTGATCG GAATCCTAAG CGGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTTGGTG	1020
	GGAGGTCTCT TTCAGCACTT CGACTACTAC AATTCGGAAA AACGAATAAG CAAAAATTTCG	1080
25	GAGGAGGTAC TCGTCACCCC ATACCGTATC TCGCAAGTGG CAGCTCTGGG AGGCGGTCTT	1140
	ATCTTCCAGC ACCACGGAAA ATTTGACGA CGTCCTCTGG AGCTATATGC CGAGACCTAC	1200
	CTGAATGTCG TCCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC	1260
	TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG	1320
	TGGAGCTGGC TCTTGGGAGT CGAAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG	1380
30	CCGCACCAGA AAAATACCGA TGTCAGCTCT TTTATGGTGC AGGGGGACGA AAGCAAGGCG	1440
	CGCCTACTGG TGACGAGTTC CGAGTTCGCA TTTATCCTG GCCCCTGGCA TGTAGCCATC	1500
	GTCGCTCGCC GTTTCATCCG CAAAACAGCC TATCAATTCT ACCCTAACGT ATCATTCGAT	1560
	ACCGGCGACA TACAGCTGCG TGTCCGATTT CACTTC	1596

35

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 5 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...900

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

	AAAAGAAGAA AAAACAGAT GAAACGACTG ATTGTTTTTC TGGCAATGGG TGGCTTGCTG	60
	TTCACCCTTG CGAACGCACA AGAAGCAAAC ACTGCATCTG ACACTCCCAA AAAGGACTGG	120
25	ACTATAAAAG GTGTGACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC	180
	GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTTGAACA TAGATGCCAA CTACCTGAAA	240
	GATAAATGGA GTTGGGACAA CGGTTTGCGT ACAGACTTCG GTCTGACCTA CACAACAGCC	300
	AACAAGTGGA ACAAAAGTGT AGACAAGATC GAACTCTTCA CGAAGGCCGG CTATGAGATC	360
	GGCAAACATT GGTACGGAAG TGCCTTTTTT ACTTTCCTCT CACAGTATGC CAAAGGATAT	420
30	GAGAAGCCCT CGGATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCCTGCA	480
	TATCTCACTC TCGGTATTGG TGCAGACTAT AAGCCCAATG AGAAGTTCTC TCTCTACCTC	540
	TCTCCTACAA CGGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTTGGGAGCC	600
	TTGCGGGTGA AAGTTGGTGA AAAGACAATG TTCGAAGTTG GTGCTTTGGT AGTGGGTTCG	660
	GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTTCTCGGCT	720
35	TATACGCACG ACTTTGGCAA CATTGACATC AATTGGGAGG CTATGCTGGC CATGAAGATC	780
	AACAAGTTCC TCACGGCTAC GATAGCCACC AATCTTATCT ACGACGATGA TGTGAAGATC	840

AACGATGGCC CGAAAATCCA GTTCAAAGAA GTTGTGGGCG TGGGTGTTGC GTACACTTTC
900

5 (2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2919 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2919

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

	TTTTACACCG GAATTGACTT GCATATAGAA AGCCAAATGA AGAAACTTTT CCCATTATTA	60
	TTACTCATAT TGTCGATTTT GGTCGGATGT GGAAAAAAG AAAAACACTC TGTAAC TGAA	120
30	ATCGCCNGAG AGAAAAAGCG TATTACTGCA TTGCTGTACG AAAAAGAACT CCCCCTGAT	180
	TCTGT TAAAC AGCTTTACGA GAACAGCGTA CAGAACAAGA ACCTTGTGGG ACAAATGTTA	240
	TTTCGCGATCG AGGTCGGCAA ACGGATGCGT AATATGTCCC AATACACAGA TGCGATGCTA	300
	TATCACCAAA AAGGGTTGAA CGCTGCATTG AATCTAAGGG ACACCATCGT AGCCGCACAA	360
	GCATGGAATC ATCTCGGAAC GGATAGCCGT CGTATCGGTG CTTTGGCAGA AGCTTCGGAT	420
35	TATCATTACA AGGCTCTTTC CTTGATAGAA TCTTTTAGCG GAAACCAGAA TAGGCCTGCG	480
	ATCAAAGCCA GATCGGCGGC CCTGAACGGC ATCGGCAACA TCAATCTTGA GTTAGGATAC	540

	CATGATGAGG	CCGAAAAGAA	TTTCCTGAAA	GCACTGCAAG	GTGAGAAAGA	ACTCGACAGT	600
	CCTCTCGGGC	AAGCTATCAA	CTATGCGAAC	CTCGGACGTA	TCTATCGACA	ACGCAAAGAA	660
	TACGACAAGG	CTCGTACCTA	CTTCCTCTTG	TCTCTGGAGC	AGAACAATAT	GGCAGAGAAT	720
	CTGATGGGTA	TCGGACTCTG	TAGCATCAAT	CTCGGAGAAG	TAGACGAAGA	AAAAGGGGAT	780
5	TATCAAAAGG	CTTTGCAAGA	GTATGCCACG	GCATACAAAC	TGATGGAACA	GTTGTCCGAT	840
	CGATGGCACT	GGCTGAATTC	CTGTATCCCG	ATGGCACGTA	TCAATCTCAA	ACAAGGTAAC	900
	GAAAGGCTCT	ACCAGCATTT	CATTTCTTTG	GCCGAAGGGA	CTGCGAAAGA	AATTAATTCTG	960
	ACTTCACATC	TGATAGAAAT	ATACAATCTT	CAATACGAGA	ATCTCGAGCG	TAAAAAAGAA	1020
	TACAAACAAG	CCCTCGAAGC	ATTCTGTCTG	AGCAAGACGT	TGAGCGACAG	CATGTCCATT	1080
10	GCGCACAAGG	TCAGCAGCAT	ACAAGAAACG	CGATTCAACT	ACGAACGAAA	CAAGTCCCAA	1140
	AAAGAGCTTG	AAGAAATACA	GCAAGTAAGC	AAGGCAAAAC	AAGAGAAATC	GAAGTTTATC	1200
	CTCTTGAGCA	CTCTTTTTGC	CCTTTTCATC	TCGATTCTTT	TGATTTCTGT	TCTGACATAT	1260
	GCATACCGTC	AGGGCAAGAA	GCATAACAAG	CTGATCAAAG	AGACGGATAA	ACTTCGCTCC	1320
	GGCTTTTTCA	CCGGTATTAC	ACACGAATTT	CGTACGCCTA	TCACCGTCAT	ACAAGGTTTG	1380
15	AATGAGAAAA	TGAGTTCAAG	TCCTGATCTC	CAAGCATCGG	ACAGAACCGA	GCTGCACAAG	1440
	ATAATAGACA	GACAGAGTAG	CCATATGCTG	AATTTGGTGA	ACCAGCTGTT	GGATATTTGC	1500
	AAGATCAGAA	GCGGAGTATC	CACGCCCCGA	TGGCGCAATG	GCGACATCGT	CTCCTTCGTA	1560
	CAGATTCTCA	TCGATTCTGT	TGCACCATAC	GCACAGGCTC	AAGACATAAC	CTTGGAGCTA	1620
	CAACCCGAGA	GCAAACCTAT	TGTCGTGGAC	TTCGTCCCCT	CCTACTTGCA	AAAAATCATA	1680
20	TCCAATCTTT	TGTCCAATGC	CATCAAGTAT	TCTTTAGCCG	GAGGGAGAGT	GGTCATATCT	1740
	CTGGCAAAAA	CCAAGAATGA	AAAAAATCTG	ATCATACGCG	TTGCAGACAA	TGGCATAGGA	1800
	ATAGATAAAA	CTGATCAGGC	TCATATCTTC	GACATCTTCT	ATCGAGGACA	GTCCGCTACC	1860
	GAAAAGCATG	GATCAGGCGT	CGGACTCTCG	TTTACCAATA	TACTGGTCGA	AAACCTTCGA	1920
	GGTACGATCA	AAGTGGAAG	CCAGCCGGGG	AAAGGAAGTG	CCTTCACCAT	CAGTATTCTT	1980
25	ACACAAAACC	AGTCCTCTTC	GGCAGAGATT	CTTCCTTGGC	TACCCCTCCTC	CGATGACATT	2040
	GTCATGCCTG	TCCACATCGC	GCCCGATGAC	TCACCGACAT	CTCCGATGGT	AGCAGCTCTG	2100
	AATCATCGCT	TCGAGGACGA	ACGTCCGACC	ATACTGCTCG	TCGAGGACAA	TAAGGATATC	2160
	AACCTGCTCG	TCAAACCTACT	CCTTTGCGAT	CGCTACAATG	TGCTATCCGC	CGCAAACGGA	2220
	AAAGAGGGTA	TAGCCCTCGC	TACCGAGCAT	ATTCCCAGCA	TTATCATTAC	GGATATTATG	2280
30	ATGCCGATAA	TGGATGGGAT	AGAAATGACA	ATCCGGATGA	AGCAATCGCC	TCTGCTCTGT	2340
	CACATTCCCA	TTGTCGCTTT	GACGGCCAAG	AGTACCGAAC	AGGACAGATT	GGAAGGAATC	2400
	AAAAGCGGTG	TAGTCTCTTA	TCTATGCAAG	CCATTCTCTC	CGGAGGAGCT	TTTGATGCGG	2460
	ATCGAGCAGC	TTCTGAAAGA	CCGTGAGTTG	CTCAAGAAGT	TCTATATGCA	AAAACCTCATG	2520
	CTGGATCGGA	AGCCGGAGGA	GGAGCCTCAA	CCGATAGATG	ACAGCAGTAT	GCAGTTTCTC	2580
35	CTTGCTGCCA	AAGATGCAGT	GTCCGGTGGA	ATCAAACAAA	ATCCGGATTT	TTCCGCTCAA	2640
	GACTTGGCCG	AAAAAATGTG	CATGAGTCCA	TCCCAACTCA	ACAGAAAGCT	CACGAGTGTC	2700

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GTAGGTTGCT CCACCATCGG CTACATACAG CAGATCAAGA TAAAATTGGC CTGCAAGCTC 2760
CTTGCCGATG AGAGCAAAAA CATCTCCGAC ATTAGCATTG AGGCAGGCTT TTCGGATCCG 2820
GCTTACTTCT CTCGCACCTT CAAACGCTAC ATGAACTGCT CTCCCTCCCA ATATCGGCAA 2880
AAACTCCTTG CCATGCCGGG GAGCGACAAG GAGACAGTT 2919

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5

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- 15 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 25 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

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30 TATAAGCAAG CTATAATGAA ACATTTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT 60
TCTTTTTTCCG GTACCTATAC CTTTGCACAA GAAAATAATA CAGAAAAGTC ACGATTTGAT 120
TTTTCTGTTA GGCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG 180
TATACATCTG CTAACGATAG ACTTTTGTCT GGTGCAATTT ATCTGGGCTT GACACCAAGT 240
AAGAAAGAAA ATGCAACCGG CGTAGCATTT CGTTTCTTAT CNCCCTCTCC GGGTTATTAT 300
35 GTCGATATAT CCGGCAAAGA AAATACCTTG AATTATGCGT TTTACGTTGT CGGAGCATAT 360
AATAGAATAG CCATTCCTAT ACGCCCTATC AAAAATTTTA ATTCATCTT CTCTACAGAA 420

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GTCGGAATGG CTTGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTTC GCAGACTTGG      480
GATAAGCAGC GCAAGTCGAG GTCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATNC      540
CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTCTTG CATGTTTCGGA      600
AAAAGGATCA ATGACTACCA GCAAAAGGAT CGAACCTTCA TTGCACTTAT CGACAACAGT      660
5  ATTGGCATAG GATTAAACCT C                                              681

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(2) INFORMATION FOR SEQ ID NO:16

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

15 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

25 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

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30 ATGAAAACAA TTAGTAAGAA CCATGCGGCA CGGATCTGTG CCGCCATTGC TTTGTTTGCA      60
   GTGTGTAACG GCCGGATAGC TGCTCAGGAT TTTCTCTATG AAATAGGAGG AGGTTTTGGT      120
   GCTGCTCAGT ATTTTGGCGA TGCAAACAGA GGCTTGTTTC GTTCATCCGG AGTAGGTTTG      180
   GAGTTGGTCG GACGTTACAA TTATAATTTT CGCTGGGCTT TCAGTACCAT GTTGGATTGG      240
35 CGTACATTGA GAGGCGATAC CGATAAGTCC GGAATGTCT TCCCCGATTT TGCTCAAGCG      300
   GATTTTAAGG TCGGCTTGAC TCAGCTCCAC GTTAGAAGCG AATTAACTT TCTCCCTTAT      360

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AGCGATGGCT ATAAGTATCT TGGTACAGCT CGGCTGTCTC CTTATGTAGC GGCCGGGTTG      420
TCTTTGGGTT TTGCTTCGGG TGCTAAAGGT TCGGCTTTTG CTCCCGGGAT TACTGCGGGA      480
ATGGGAGTGA AGTATAAGCT TAAACCGCGG ATCAATGTCTG GTATCGAGTA TTCTTTCACG      540
GGGTTACTTA CCGATGCTTT GGATGCGCTG ACGGATAAAA GTGTTTGGCT CGAGGATCCA      600
5  TATAAGATCA ATGACTCCTG GGTCAAAAAC AAGGATGCTA CAGGGGCCTT AGTGCTTAGG      660
ATTACGTATG ACTTCGGCCT GCGTAAGACT TTTTGTAAATA AACAA                      705

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(2) INFORMATION FOR SEQ ID NO:17

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

25

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3486

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

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GCTATTTCTC AGATGAAACG AATACTTCCA ATAGTCGCAT TCCTTTCTCT CTTCTTGCC      60
CTTGCTTTGC CTGCGAAAGC GCAACGAGCT ATGGGGAAGA CGGCCGACCG TTCGCTAATG      120
GCTTCGGGAC ATTGGGTCAA GATACGTGTC GATGCAAGTG GAGTGTATCG CCTTACGGAC      180
35 GAACAGCTCC GTGCCAATGG CTTCTCCGAT CCGTCCAAGG TAGGTGTGTT CGGTTATGGT      240
GGAGGGGTGC TTCCCGAAGA TCTGAGCCGG ATCACGACAG ACGATTTGCC TCCGGTACCG      300

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	GTACTCCGTC	AGGGCAATGC	GCTGTATTTT	TATGCCGTGG	GCCCGGTGAC	ATGGTTCTAC	360
	AATCCGGCCA	AAACCACCAT	GGAGCATACG	GTGAATACAT	ACAGTACGCA	TGGCTACTAC	420
	TTCCTGTCGG	ATGCTGCCGG	AGCACCTTTG	CAGATGTCCC	AATATACGGG	TGGAGGTGCG	480
	TCGGCCGAGG	CTTTGATCGA	CTACTACGAT	GAGCTGATGC	TCCATGAACA	GGAATTGTAT	540
5	TCGCCCCAAG	AATCGGGACG	AGATCTGTAT	GGCGAGTCTT	TCAGTGCAGT	CAATACGCGT	600
	ACGGTCAAGT	TCCCTTTGAG	GGGCAACACC	CGCTCGTCTG	GCGAACTCGG	TACCGTATTC	660
	TCATACATAG	CCAAGGCCAG	ATCGGCCGGT	GGCGGCCGTG	AGATGTCGCT	CTCGGCCGAAT	720
	GGCATTCTGA	TCTTCAGCGA	TCCTTTTTTC	ATGACATCGA	ATGAAGTCTC	CAATTCCTAT	780
	TTGGCCGGCA	AGAAGCGTCG	TCTCTATCAC	AGTACGCCGA	TGAACAGCTT	GGTCAATGAG	840
10	TTGCGCTTGG	ACGCGAACTA	TAGCATGACA	GGAGATGCGG	TCAATCTGGA	TTTCATAGAG	900
	GTGGCTACAC	AGAACGACCT	CCGGTACGAT	GGCGCACCCA	TGCATATCAG	GCGGTTTTTC	960
	AATTTGCCCC	TTTTGGGGGG	CGAGTCCTGC	CGGTTCGTTA	TCAGTGAGGT	GCCGGAGTCT	1020
	CTGGTGGTTT	TGCAGGCCAA	TTCTTCCCTG	ACAGCATCGC	TTGTTCCCGT	TAAGACTGTC	1080
	GGGGATAAGA	CCATTGAGTT	CGTGGCTCCG	CCGAAGGGTC	AGGATCGTAG	GACTATCAAT	1140
15	ACGTTTTATG	CCGTGGACTT	GTCACAGGCT	TCTGCTCCGG	AGATCCTCGG	AGCGGTACCC	1200
	AATCAAAACC	TGCATGGAGA	GGAAATCCCT	GATCTGATCA	TTGTCTCTAC	TCAGGCGCTC	1260
	CTCCTTGAGG	CTGATCGACT	GGCCACCTAT	CGTAGAGAGA	AAAACGGGCT	GAAGGTTTTG	1320
	GTCGTGTTGC	AGGAACAGGT	GTTCAACGAG	TTTTCGGGTG	GAACCTCCCA	TGCTACAGCA	1380
	TACCGCCTCT	TTGCCAAAAT	GTTCTACGAC	AGATGGAAGG	CAAATGCACC	TGTGGGAGAG	1440
20	ACCTTCCCGA	TGCAAATGCT	TCTCTTCGGT	GATGGGGCTC	ATGACAACAG	GAAGGTCTCC	1500
	GTAGCTTGGC	AGAAACCGTA	TCTCCAACAA	ACGGAGTTCT	TGCTGACATT	CCAAGCCGTC	1560
	AATTGACGCA	ACGTAAACAG	TTATGTGACG	GATGATTACT	TCGGCTTGCT	GGATGATCAG	1620
	CCGGCCTCGG	TCAATATCGG	TTGGCGCAAT	TATAATATGG	CTGTAGGGCG	ATTCCCCGTA	1680
	CGTACTCCGG	CCGAAGCTCG	CATCGCAGTG	GACAAGACCA	TCCGATATGA	GGAGGATCGA	1740
25	GAGAGTGGTG	CCTGGCGTAT	TCGTGCCTGT	TTTGCGGCAG	ACAACGGGGA	CAAGCACGCA	1800
	ACCGAGACTT	CCCGTTTGAT	CGATACCGTC	AAGCGTTATG	CTCCTGCCAT	CATGCCGGTA	1860
	CGCGCCTTTC	AGGACGTATA	TCCGCATGTC	ATCGAGAACG	GGTTGCACAG	CATTCCGGGT	1920
	GCAAAGAAAA	AGATGCTGGA	AACCCTTCAG	TCGGGTATTA	TCCTGCTTAA	TTATGCTGGT	1980
	CATGGCGGTC	CTGCCGGATG	GTCGGACGAG	CATTTGCTGA	CGCTCAACGA	TATACACAAA	2040
30	TTCAATTATA	AGCATATGCC	CATTTGGATT	ACTGCCACGT	GCGACTTTGC	CAACTATGAC	2100
	AGTCAGACGA	CCTCGGCAGG	GGAGGAGGTT	TTCTCCATG	AGAAGAGTGG	CACTCCGATC	2160
	ATGTTCTCGA	CTACGCGTGT	CGTTTACAAT	ACGCAGAATG	AGAAGATCAA	TGGTTTTATG	2220
	CTTCGGCGTA	TGTTTCGAGAA	AGCTAAGGAT	GGGCGTTATC	GTACGATGGG	CGAGATTATC	2280
	CGATCGGCCA	AACAGGGGAT	GCTCAGTACT	GTTTTCCCCG	ATTTCGATCAA	CCAGTTGAGT	2340
35	TTCTTTCTGA	TGGGTGATCC	GTCCGTGCGT	ATGAATCTTC	CTACCCACAA	AGTGCAATTG	2400
	ACCGCAATCA	ACGGGCAGGA	TCCCGAAGGG	CAGTATGGAA	CTATTATGCT	CAAGTCTTTG	2460

	GAACGGGTAG CTCTGAAGGG TAAGGTAACC GATGAAAAGG GGACATTCTGA CGAGACATTC	2520
	AGTGGCAAGG TTTTCCTGAC CGTCTTCGAT GGCAGAAAGA AAATGACAGC TTTGGAAGAG	2580
	GAGGGAAACG ATCTCTCTCT TGTATATTAT GACTATCCTA ACGTGATGTA TGCCGGTATT	2640
	GCCGAGGTGA AAGACGGACT CTTCGAAACT TCGTTTATCG TACCCAAGGA TGTGAACTAT	2700
5	TCCGAGCACG AAGGCCGGAT CAATCTTTAT GCTTATAACG AGAGCACAAA GGCGGAAGCC	2760
	ATGGGGGTAG ACTTCTCCAT CAGAGTCCAA CCGGGTATTC CTGATGAGGT AACGGAAGAT	2820
	AATACACCGC CTGAAATCAT AAGCTGCTTC CTCAATGACA GTACATTCCG ATCGGGAGAT	2880
	GAGGTTAATC CTACTCCTCT GTTTATGGCC GAAGTATTCG ACTTGAATGG AATCAATATC	2940
	ACGGGTAGCG GAGTAGGGCA TGATATTACG CTTTGTATCG ATGGCCGTGC CGACCTGACC	3000
10	TACAACCTCA ATGCATATTT CACAAGTTCG GCTACGGATG CAGGTGTGGG CACTATTCTC	3060
	TTCATGATAC CGGCTTTGGC CGAAGGAGAT CATACTGCCC GACTGACGGT TTGGGACATT	3120
	TTCAATAATG CCGTCCATCA TGACTTTTCA TTCAGAGTGG TAGATGGCAT TGCTCCGGAT	3180
	GTGGCTGATG TGATTCTATT CCCGAATCCG GTACGCGAGA GTGCTACGTT CCGAATCTTC	3240
	CACAATCGCC CCGGAAGCGA TTTGAACGTG GCCGTGGAGA TCTATGACTT CACCGGTCGT	3300
15	CTTGTGAACA GTTTGCCAGT CAAGACCTAT TCGTCTTCCT ACGGAGAACC TATAGAGATC	3360
	AAGTGGGATC TGACCTCCAA ATACGGAGTG AAGATCGGAA ACGGATTCTA CCTCTATCGT	3420
	TGTGTGGTGA ACTCTCCCGG AGGACAGACG GCCTCCATGG CCAAGAAAAT GATCGTGGTA	3480
	GGACAA	3486

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(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|-----------------------------|
| | (A) LENGTH: 1218 base pairs |
| 25 | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: circular |

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1218

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

	ATATTCATAG ACCCCGATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA	60
	ATGCTGAAAA ATAAATTGGC CCCCTTGGCC ATACTGTTCC TTTTGTGCTCC AAAGGCTATG	120
10	AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG	180
	GATGCACGTG CGGCCGGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TGC GTATTCA	240
	CAGTATTGGA ATCCGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA	300
	TATACACCCT GGCTGTCCAA GCTGGTCAAT GATATTGCCC TGATGCAGAT GACCGGTTTC	360
	TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA	420
15	GGAAAGTTGG AGACTTTCGA CGAATTGGGC GAATCCATGG GAGAGGCCCA TCCCAATGAA	480
	TTTGCTGTCG ATTTGGGCTA TAGCCGCCAG TTGTCGGAGA ACTTCTCCAT GGCTGTTGCA	540
	CTGCGTTACA TCCGCTCAGA CCAAAGCACT CACAACACCG GAGAGAATCA GGCCGGAAAT	600
	GCCTTTGCGG CGGATATAGC CGGTTATTTG CAGAAGTATG TGCTACTGGG TAATGCGGAG	660
	AGCTTGTGGT CGTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA	720
20	GGTGTACGA GTTTTTTCAT CCCTACTTCG TTGAATCTCG GGACGGGGCT GTTGTATCCG	780
	ATCGATGACT ATAACAGCAT CAATTTCAAC CTTGAACCTA GCAAGCTGCT TGTACCCACT	840
	CCTCCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG	900
	GAAACTTCTT CGATCAGCGG TATATTCTCT TCTTTCGGTG ATGCGCCGGG AGGACTCAAG	960
	GAAGAATTCC GTGAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA-CGATAAATTT	1020
25	TTTGTTTCGTG CCGGATATTC ATACCTGCAC CCCACCAAAG GCAATTTGCA GTACTTCACG	1080
	GCCGGTGCCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCTACCT GTTGTCTACG	1140
	ATCCAGAGTA ATCCGTTGGA TCAGACTCTG CGGTTTACGC TTGCTTTCGA TATGGATGGA	1200
	TTGCGCAATT TGTTCCAC	1218

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(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...663

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

	ACGAGAGAGA GTGTGTTACA TTGTAGAACA AAACCTCAAAA AAGAACGAAA AATGAAGAAA	60
	ATGATTTTGG CAGCTACTAT GCTGCTCGCA ACAATCGGTT TTGCAAATGC TCAGAGTCGT	120
20	CCTGCTCTTA GACTGGATGC TAACTTTGTC GGTAGTAACT TAATGCAAAA AGTCGCAAAC	180
	ACGAGCGTGA ACAATAAGAT GATCGTAGGC TTACGTGTTG GTGCTGCTGC TGAGTTCGCT	240
	CTTAGCAATG ATGGATTCTA TCTCGCCCCC GGATTGGCCT ATACGATGAG AGGTGCTAAG	300
	ATGGAATCAC TAAGTGAAAC GACAACTCGC TTGCATTATC TGCAAATACC GGTGAATGCC	360
	GGTATGAGAT TTAGCTTTGC TGACAACATG GCTATTTTCAT TGGAAGCAGG-TCCCTATTTT	420
25	GCATATGGTG TCGCCGGAAC GATTAAGACT AAAGTTGCAG GCGTTACGGC TTCTGTAGAT	480
	GCCTTTGGTG ATAACGGATA TAACCGTTTC GACTTGGGCT TGGGCTTGTC TGCTGCCTTG	540
	AGCTACGACC GTTATTACGT ACAAATTGGA TATGAGCATG GATTGCTTAA TATGTTGAAG	600
	GATGCTCCGG ATAAGACTTC TTTGCGTAAT CATGACTTCT TTGTGGGTCT CGGTGTTTCGC	660
	TTC	663

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(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

	AAAGGTACGT GGAATAGAAA AAACCGAAGA GAAGAAATGA AACGGACAAT CCTCCTGACG	60
20	GCACTGACCG TCCTATCTTC GCTCTCCTTG CTTCGTGCAC AAAATGAATC CGAAGCATCA	120
	ACCAATCCGA TGTCAGGCCT CTCCCTGGAA GACTGTATCC GGATAGCCAA GGAGCGCAAC	180
	CTGAATCTGC GCAGACAGGA GATCGAACAA GAAAACCGAA TCATTAGTCT CGATGCAGCA	240
	CGACACAGTT TCCTGCCCTC GGTCAATGCA GGCATCGGAC ACAACTATAG CTTCGGACGT	300
	TCGAAAGACA AAACGGGAGT AACCGTAGAT CGCTCCTCGA TGAATACCAA- TCTCAGCATC	360
25	GGAGCTTCGG TGGAAGTATT CAGCGGCACA CGTCGTCTGC ACGACCTCAA GCAGCAAAAG	420
	TACAACGTGG AGGATGGTAT AGCCCGACTT CAAAAAGCGC GTGAAGACCT CAGCCTGCAA	480
	ATCGCGGCTC TCTATATCAA TTTGCTCTTC CGTCAGGAAA TGAATCGTAC GGCAGAAACA	540
	CAGTTGGCAC TGATTGCGCA GCAACGCAAT CGCACGGCCG AAATGGTTCG CGTAGGTAAA	600
	TGGGCAGAGG GTAAGCTCCT CGACATAAAT GCCCAGATGG CCAAGGACGA ACAACTTCTC	660
30	GTACAAATATC GTTCGGAGGA GGAGCTGGCT CGTCTGGACT TGGGGCAAGC CCTCGAACTG	720
	GAGCACCCCG AAAGCATTCG AGTCAAGGCT CCCGACACAG ACGTTCTCGT AGCAGAAAGG	780
	TTGGGATCTC TCCTTGCTCC CGAAGAGATC TATCGCACGG CTCTCGGCTT GAAACCGGCA	840
	CTGCATTCTG GCGAGCTGCA AATAGCTTCG GCACGCGAAG GTCTGGCCTC GGCTCGTGCG	900
	GCATACTTCC CGACGCTCAG CCTCTCTGCC GGATACAGCA ACGGTTACTT CCGCGACCTC	960
35	GGCAAGGAGT ATGCCGCCAT CAACCCCTCC TTCTCCGAAC AGTGGAAGAA CAACGGCAGC	1020
	TACAGTATCG GACTCTCTTT GAATATCCCC ATCTTCTCTG CCATGCAAAC GCAAGATCGC	1080

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GTTTCGGAGCA GTCGCCTGCA AATACGCTCA AGCGAGCTTC GACTCGTCGA AGAGAAAAAA 1140
GCCCTCTATA AAGAGATCAG GCAAGCATAC AGCAATGCCG TGGCAGCCGA TAAGGCCATC 1200
GCAGCAGCCG AAAACAGCAA GGCCGCTACG CTCAAGGCAT ACGAATACGC TCGCGACAGC 1260
TTCGAGGCAG GGCCTTGTG TGCCTACGAA TATGCCGAGG CAAAACAAA ATACGCCCTC 1320
5 AGCCAAGTGG AAGAACTTCG TGCCAAGTAT GACTTCATAT ACAAAGCCAA AGTTTTGGAT 1380
TTCTATCAGG GCAAAGACTT C 1401

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(2) INFORMATION FOR SEQ ID NO:21

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

25

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1308

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

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AATATAATGT ATAAAGACTA TAAGGGTTTG TATGCGTCGC TTCGGTGGTA TGCCCTGATC 60
ATTGGGTTGC TATTTGCAGC AGACGGTATA CAGGCTCAGA ACAACAACCTT TACCGAGTCG 120
CCTTACACTC GCTTCGGCCT TGGCCGTCTC GGAGAACGGA CGACTATTAG TGGGCATTCC 180
35 ATGGGAGGAC TCGGCGTCGG TCTGCGTCAG GGCACATACG TCAATGCCGT CAATCCTGCT 240
TCATACTCGG CTGTGGATTC GATGACGTTT ATCTTCGATT TCGGTGCATC TACCGGAATT 300

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ACGTGGTATG CCGAGAACGG GAAAAAGGAC AATAGGAAAA TGGGAAACAT TGAGTATTTTC 360
 GCCATGCTTT TTCCTATTTT CAAATCCATT GCTATGAGTG CGGGAGTGCT TCCTTACTCC 420
 GCATCCGGGT ACCAGTTCGG ATCCGTTGAT CAAGTGGAAG GAGGCAGCGT CCAGTACACC 480
 CGTAAATACT TGGGGACAGG CAATCTGAAC GATCTCTATG TCGGTATAGG TGCAACCCCG 540
 5 TTCAAAACT TCTCAATAGG AGCCAATGCT TCATCCCTTT TTGGGCGATT CACACACAGC 600
 AGGCAGGTAA TCTTCTCCAC GGAGGCTCCT TACAATCCCG TACATCTCTC GACGCTGTAC 660
 TTGAAGGCTG CCAAGTTCGA CTTGCGTATG CAGTATCACC TTCTTCTCAA ATCAGATCGT 720
 TCGCTCGTTA TCGGTGCCGT CTATTCTCCG CGGGTGAAGA TGCATAGCGA GCTGACTCAG 780
 ATAAAGAATC AGGTTCAGAA CGGTGTAGTA GTGGAGAGCG AAACCCAAGA ATATATCAAG 840
 10 GGAATGGACT ATTATACCCT GCCTCATACA TTGGGGATAG GTTTTTCTTA TGAAAAGAAA 900
 GATAAACTTC TCTTAGGAGC AGACGTCCAA TATAGTAAAT GGAAAGGCGA GAAATTTTAT 960
 AAATCCGATT GCAAATTCCA GGACAGAATA CGGGTATCTC TCGGCGGAGA GATCATACCG 1020
 GATATAAATG CCGTTGGGAT GTGGCCTAAA GTTCGCTATC GCTTCGGTTT ACATGGTGAA 1080
 AATTCTTACC TGAAAGTGCC GACTAAAGGC GGTGTATATC AAGGATACCA TATCGTAGGT 1140
 15 GCTGTATTCTG GTATAGGAAT CCCGCTCAAT GACAGACGTT CGTTCGTAAA TGTCTCTCTT 1200
 GAATATGACC GATTGATCCC GAAGGAGGGT ATGATCAAAG AAAATGCTCT GAAATTGACC 1260
 TTCGGCCTCA CGTTCAACGA GTCATGGTTT AAAAAGCTGA AACTGAAC 1308

20 (2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2835 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2835

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

	AATACCATTT	CGGAGAATGG	GAACGATAGC	ACCTATTTTT	CTTTTCAAAC	TTTTCTTATG	60
	CGATCGATTT	ATCAATTACT	GTTGTCAATA	CTCCTTGCTT	CTCTTGGTTT	CGTCGGGCTG	120
	GAAGCCCAAC	AAGCCGGAGT	AGCAGGTAGA	GTATTGGACG	AAGAAGGCAA	CCCCATGATT	180
10	CAAGCCAACG	TACAGCTTGT	ACAGAGTACC	GGCCAAGTAG	CCGTTGCCGC	AGGTGCCACT	240
	AATGAAAAAG	GGTTGTTTCT	CCTGAAAACG	TCACAGGAGG	GTGACTACAT	TCTGCGCGTT	300
	TCATATGTAG	GTTACACTAC	CCACGACGAA	AAAATATCTC	TTAGAAACGG	GCAAACCATT	360
	ACGCTCAAAG	ATATATCCAT	GAACGAAGAT	GCCCGTCTTC	TACAGAGTGT	GACGGTGCAG	420
	GCTAAAGCGG	CAGAGGTCGT	GGTACGCAAC	GATACGCTCG	AATTCAATGC	CGGATCCTAT	480
15	ACCGTAGCAC	AGGGAGCTTC	TATCGAGGAA	CTGATCAAGA	AGCTACCCGG	AGCAGAGATC	540
	GGATCCGATG	GGAAGATCAC	CATCAACGGC	AAGGACATTA	GCAAGATCCT	TGTCGATGGC	600
	AAAGAGTTTT	TCTCCAAAGA	TCCACAGGTG	GCAATAAAGA	ATCTTCCGGC	CGATATGGTC	660
	AATAAAGTAC	AGGTACTGAA	CAAACTGAGC	GAGCTGTTCG	GGATGAGCGG	TTTCGATGAT	720
	GGAGAAGAGG	AGACCGTAAT	CAACCTGACG	GTGAAGCCCG	AAAAAAGAA	AGGCCTCTTC	780
20	GGAACGCTTC	AGGCCGGCTA	CGGTACCGAC	CAACGCTATA	TGGCCGGAGG	GAACGTCAAT	840
	CGGTTCGATG	GAAATAAGCA	ATGGACATTG	ATCGGTAGTG	CGAACAATAC	GAACAATATG	900
	GGCTTTAGCG	AGATGGACAG	CGAGATGGGA	TCCATGACCT	TCTTCTCTCC	CCAAGGCGGT	960
	GGTCGACGCG	GCTTCGGCAA	TAGTGGAGGT	GTTACGTCTT	CGTCGATGCT	GGGCGGCAAC	1020
	TTCACTGTCT	AATTCTCCTC	TGCCCTTAAT	ACAGGAGGCG	ATGCACGCTA	CGGATACAAC	1080
25	GACAAGGCCA	TAGAGACGAC	CAAACGCGTG	GAAAAATATCC	TCGCCGAAGG	GAATACTTAT	1140
	ATGGACGAAA	ATATATTGGA	ACGCTCTTTC	TCTCACAATG	GTCAGGCGCG	ATTTAGGATG	1200
	CAATGGAAAC	CGTCCGAACG	TACCGAAGTG	GTATTTCGAGC	CGGATCTTTC	GATATCCAAG	1260
	ATCGATGGGT	TCTTTAACGA	CACATACGAG	ACGAAAGATG	CCACCGGAAT	CTCTATCAAC	1320
	AAAGGTTCTA	TCCACCAAAC	TACACAAGGA	AACAACTTCA	GACTGAACGG	AGAATTGGAT	1380
30	ATCAGTCACA	AGCTCAACGA	CGAAGGCCGT	ACGATCAGTG	CCTCCGTCAG	TGGCGGTCTG	1440
	ACCGACGAAG	ACGGAGATGG	CATATATCAG	GCTGTGCTCC	AAAGCGTGGA	GACGAATCAA	1500
	AAGCAATTCA	ACGACAACCT	CAACCTGCAA	TATCGGCTTC	GCCTCTCGTA	TGTGGAACCG	1560
	TTGGGTAAAA	ACTACTTCGC	ACAAGCGATT	CTGAACAGAC	GTTTCTCCCG	TCGCAATTCTG	1620
	GATCGTGAGG	TGTACCGACT	GGGCGATGAC	GGGCAATACT	CCATATTAGA	CAGTCAGTAC	1680
35	GGACTCTCCT	ACAGTAACGA	GTTCACCCAG	TATCGCATCG	GACTCAACCT	CAAGAAGATT	1740
	GCCAAAACGT	GGGACTACAC	CGTAGGATTC	AATGTGGATC	CCAACAGAAC	TGTCAGCTAT	1800

	CGGAGCGTAG CCGGAGTAGA GCAGGACAAA CTGGCTTTCA ATCGTGTCAA TCTCTCCCCG	1860
	ATGCTCCGAA TCAACTACAA ACCGAGCAGG ACTACCAACC TCCGAGTGGA CTACCGAGGA	1920
	CGCACGACAC AACCATCCAT CAATCAGATC GCTCCCGTTC AGGACATCAC GAATCCGCTA	1980
	TTCGTGACGG AAGGCAATCC CGGTCTGAAG CCGAGCTATT CCAACAATGT GATGGCCATG	2040
5	TTCTCGGACT TCGATGCCAA AAGTCAGCGA GCTTTCAACA TTGTTTCTT CGGCAACTAT	2100
	ACATTGACG ACATCGTCCC CAATACGCAC TACGATCCGT CTACAGGGAT CCGTACCACT	2160
	CGTTACGAAA ACGCCTCCGG TACGTGGCAA GCGAATCTTC ATGGGACACT ATCGCTTCCA	2220
	CTCAAGAACA GGGCATTTTC TTTCAGGATG TCCTTGTTCA ACAGGTGGC CGAAGGACAA	2280
	AGCTTCATCA ATGACGATAA GAACAAAGCT CTCTCTTCC GAACGAGGGA ACGCCTGACG	2340
10	CTGACCTATC GCAACAATTG GATCGATACG AGTATCGGTG GCAATATCGG ATTCTATATG	2400
	GCGAATAATA GTCTGAGCGG ACAGAAAGAT TCTCGCACAT ACGATTTTGG CGGCAATTAT	2460
	CAAGTTGCCC TAACGCTTCC CTATGGATTC CGTATCGACA GCGATGTTGA ATACAATACG	2520
	AACTCCGGTT ACAGCGGAGG ATTCAGTCTG GACGAATGGC TTTGGAATGC TTCGCTTTCA	2580
	TACAGCTTCC TCCGTGACAA GGCCGGTACA CTGCGTGTCA ATGGCTATGA CATCCTCGGT	2640
15	CAGCGGTCAA GTATCAGCCG TTCTGCTTCG GCCATCAATA TAGAAGAGAG CATGTCCAAT	2700
	ACGATCGGAC GCTACGTGAT GGTGGACTTT ATCTACCGAT TCAACGCCTT CAGTGGTGGT	2760
	GGATCTCGCA GCGATCATCA GCGTGGCAAT ATGAATCGTC CGGGCCCACC TTTCGGCGGT	2820
	GGCAGACGAC CGTCC	2835

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(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

25

(ii) MOLECULE TYPE: DNA (genomic)

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2370

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

	CTCTTGTTTT	CTTCTCCTTT	ACCCCGAATG	GATCGTCCTA	AGCCTTCATA	TATTGTTCTGA	60
	ATAGCAGCCA	TTCTCTGCTT	GTTTGTCTGGC	AGGCCTTTGT	TTGCGCAGAG	CTATGTGGAC	120
10	TACGTGCATC	CGCTGATCGG	GACGCTAAGT	TCTTTTGAGC	TGAGTGCGGG	CAATACCTAT	180
	CCGGTGATCG	GTTTACCGTG	GGGAATGAAT	AGCTGGACAC	CGATGACCGG	TGTACCCGGT	240
	GACGGCTGGC	AATATACCTA	CTCGGCACAC	AAGATTCTCG	GATTCAAACA	GACCCACCAA	300
	CCCAGTCCTT	GGATCAACGA	CTACGGCCAA	TTCTCCCTTC	TTCCCTTAC	GGCACCGCAG	360
	AAGCCATCAT	CGAACGACTC	CATAGCTCTG	ACTAAATGGT	GCAAGCAACT	CTTTTCGGAC	420
15	GAACAGACCT	CGTGGTTCTC	GCACAAAGCG	GAGACGGCGA	CGCCATACTA	TTATAGTGTC	480
	TATTTGGCCG	ATTACGACAC	ACGCGTGGAG	ATGGCTCCGA	CCGAGCGTGC	AGCTATCTTT	540
	CGCATACGTT	ATTCCGGCAA	TACCGAAAGT	GGCTCCGGTC	GATGGCTTCG	TCTTGATGCC	600
	TTTACCCGGT	GTTCCGGAGAT	TAGCATCGTG	GATCCTCACA	CCGTAGTGGG	CATATCTCGC	660
	AAGAATAGCG	GAGGTGTGCC	GGCTAACTTC	GCCTGTTATT	TCATCCTGCA	GTCCGATACT	720
20	CCTATGGCCG	ATGTCCTGCT	TGAGACAGAT	ACCGGCAAGT	CAGACGAAGG	CACAAGGGCA	780
	TGGGCAGCCT	GTCGCTTCGA	TTCGCAAGAA	GTTACCGTCC	GGGTGGCATC	TTCTTTTATC	840
	AGTGTCGAGC	AGGCCGAAAG	AAATCTTGCG	GAAGTCAAAG	GGCAGAGTTT	CGACCGGATC	900
	AGACTTGCCG	GTCGCGAAGC	TTGGAATAAG	GTGCTCGGAC	GCATACATGT	GGAAGGAGGA	960
	ACGAAGGATG	AGCGCACTAC	ATTCTATTCC	GCACTCTATC	GCTGTCTGCT	TTTTCCCCGT	1020
25	CGCTTCTATG	AGGAGGATGC	TTCCGGCAAT	TTTGTGCATT	ACAGCCCCTA	CAATGGAGAG	1080
	GTACTTCCCG	GTTATCTCTA	TACCGATACC	GGATTTTGGG	ACACTTTTCG	AGCCCTTTTC	1140
	CCCCTGCTCA	ATCTGCTGTA	TCCCGATGAA	AACATTAAAA	TTCAGGAAGG	TCTGCTGAAT	1200
	GTATATCGCG	AGAGTGGCTT	TTTCCCCGAA	TGGGCCAGTC	CGGGCCATCG	GGATTGTATG	1260
	ATAGGCAACA	ACTCTGCTTC	TGTTCTGGCG	GATGCCTACC	TCAAGGGTGT	TCGGGTAGAA	1320
30	GATACCCGTA	CACTGATGAA	CGGACTCTTG	CATGCTACGA	AAGCCGTCCA	TCCGAAAATC	1380
	TCCTCCACGG	GTCGCAAAGG	TTGGGAGTGG	TACAACTCCT	TAGGTTATGT	TCCGGCTGAT	1440
	GCAGGCATCG	ACGAAAGTGC	TGCCCCGTACG	CTCGAATATG	CTTATAACGA	TTGGTGCATC	1500
	CTCCGACTGG	GGCGCACATT	GGGTTGGGAT	AGAGCTGCAT	TGGACACGTT	GGCTCATCGT	1560
	TCGATGAACT	ATCGTCATCT	GTTCGATCCG	GAAACCAAAC	TCATGCGCGG	TAGAAATCAG	1620
35	GATGGTAGTT	TCCGGACACC	TTTTTCCCCT	TTCAAATGGG	GAGATGTATT	CACGGAGGGC	1680
	AATGCCTGGC	ACTACACTTG	GTCGGTCTTT	CATGATGTGC	AGGGGCTTAT	CGACCTGATG	1740

GGAGGAGATC GCCCGTTCGT GTCTATGCTC GATTCGGTAT TCAATACTCC TCCTATGTTC 1800
 GATGAGAGCT ATTACGGATT TGTCATCCAC GAAATCAGAG AGATGCAAAT AGCGGATATG 1860
 GGCAATTATG CTCATGGCAA TCAACCCATA CAGCATATGA TATATCTGTA TAATCATGCC 1920
 GGTCATCCAT GGAAAGCTCA GGAGAGACTA CGCGAAGTGA TGGGGCGGCT CTATCGTCCT 1980
 5 ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTTC 2040
 TCTGCTTTAG GCTTCTATCC TGTTACACCC GCTACGGATC AGTATGTGCT CGGTTGCGCCG 2100
 ATTTTTTCCA AGGTAATACT CTCTTTTCCC GACGGACACA AAACGGTGTT GCATGCTCCG 2160
 GCCAACAGTG CCGATACGCC TTACATCCGC TCGATCAGCG TAGAAGGAAA AGAATGGAGC 2220
 TGCAATTACC TGACTCACGA ACAGCTTCGC TCTTCTGCAT CCATTCAATG GATGATGGAC 2280
 10 ACGAAACCCA ATTATAATCG TGGTATGAAG GAAAGTGACA GACCTTATTC CTTCTCCACG 2340
 GAGCAACAGC GTCGCGCTAA TCACAGTAAT 2370

(2) INFORMATION FOR SEQ ID NO:24

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1356 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

30

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1356

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

	CTAATAATCG AAAAGGAAAT GAAAACAACA GTTCAACAAA TTATTCTGTG CCTGGCTTTA	60
	ATGATGTCAG GTGTATTGGG CGGAAACGCA CAGAGCTTTT GGAAGAAAT AGCTCCTCCT	120
	TTTATCAGTA ATGAGCCTAA CGTCAAGTAT ATAATTCCCA ATATGGGGAT TGATTCAAAG	180
	GGAACAATCT ATGTAACCGT GACAAAAAGG ATTCAGCAGG GAGCAAATTA TACTTCTGAG	240
5	CAATTGGGTA TGTACTATCG ACCATTAGGT GATAATGAAC AGTGGTGGAA ACATGATCCG	300
	TATTTTGATG ACAAGATAGT TGC GGATATT CAGACAGATG CATATGGCAG AGTTTATGTA	360
	TGTACGACTT CTTCTCGAGA TCAAGAGTAT CAACTTTATA TAAACGAGCA GAACGAATGG	420
	AGGTGTATAT TCAAACTTC TGTGTCTACA TATGAGCATG GTATGGCTGT TTTTCGCTCT	480
	TCGACAGGGG TGA CTTATAT AGGTACCAGG CATCACATCT TCGCATCAGG TGTAATGAT	540
10	TTGAGTTCA A CACTATCTA TGAAGACTCT ACACCTATGA GCTGTCGCTT TGCAGAGGCT	600
	ACGAATAGTG GCACCATCTA TCTGGCATTG ATGCATGAAA CCACAATGTC TACGACTATC	660
	CTTACTTATC AAAACGGTGA GTTCGTCGAT ATCTCGGAAA GTGAATTGAG TAACTCGATT	720
	ATTGCATCCA TGTGCTCTAA TAAAGAAGGT GATATAATAG CTCTTGTTAC TTCATATACA	780
	GGATTTATGA GTGGAACCCT TGCGATCAGA AAAGCAGATG AAGGCAAATG GCAACTTGTT	840
15	GGCGGAGATA TACAGAATGC GATCGTTCAA AATATATGCA TGATGGACGA CAACAAGATT	900
	GCTTGTGAAG TCTTCGGGAC TCCTAACGGA GTAGATGGTC GGACAAGGGT TTGTGTTTCT	960
	GACGCATCTG TCTTTGATTT TGAGTGGTAT GAAGATGAAA TATACGGAGG CCTGATATTT	1020
	GACACTTTCT TCTATAGCCC TTGGGACAAA CTTCTTTATG CGAAATTTGG TGGGATTATG	1080
	CTCAGGAGTA AAGAGTCTTT TATAACCTCT TTCATTTCTC CGACAGTTGT ACAAGGAGTG	1140
20	GATGTCTATA CTTTGGCCGG GAAGATAAGG ATCGAAAGTG AAACCTCCGGT GTCTGAGGTG	1200
	TTGCTTTTCG ACCTGGCTGG CAGGATGGTA CTTCCGGCAA CCATTGATAA TAAAATCTAT	1260
	TCGGACATAG A TACTAACGG ACTAAAGCGA AGCGGTATTT ACGTAGTCTC GGTGCGGCTC	1320
	TCTTCCGGAC AGGTATT CAG TCATAAGGTG CAGGTA	1356

25

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...993

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

	GGCCTGTACG GTATGTCTGT TGTACCTATA ATAATTTATC TTTGCGGTAT ATCAAATTAT	60
	GCAAGACTCA TGATAATCCG GTGTCTTATC CGTCGTC CGA GAACCGTCCT GTTCGGGTTG	120
15	ATATTCGTGG TAGGTCTTTT CTCTGCGATG GCGCAAGAGA AAAAGGATAG TCTCTCTACG	180
	GTTTCAGCCAG TGCCGAATAG CAGCATGGTG GAGCAGACCC CTCTTCTCTC CATTGATCAC	240
	CCCGTCCTGC CCGCTTCTTT TCAGAATACC CGTACACTGA AAAGGTTTAG AGACAAACAT	300
	CTTTCCGATG CTTTGCTCAA TGGATTGAAG CCTCATCGCT CATCTTTGCA ATTGAATGAG	360
	GAACTCAACT TCGCGGCAGA GCGTCGGGAT TTCGTTTCTC CCCTCTTGCA AACTCGCCAC	420
20	GCTGCCGGTG TCCTTTCATG GCGACCGACC GATAGGATGC ATTTTATAC ATCGGGCAAT	480
	ATCGGTCTTG GCCATGATTT ATTGACCGGT GTGCGCAAGG ACTTCGGATG GAATGCTGGT	540
	GCCGACTTCT TGCTGAGTCA AAATCTTACG GCACATGTCC AAGGCGGTTG GCAGCAGAAT	600
	TTGCGCTTTA TACCTATGAC GGCTGTCAAT GGCCAACTGC GTTGGCAAGC CACCGAGAGA	660
	TTGAGTTTAA CCACCGGTAT CGATTATCGA CAGGTACAGT GGAATGCTTT CGATAATAGA	720
25	ACGTTCTCGC TTAAAGGAAG TGCTCGATAC GAAGTGATGG ACAATGTCTT TGTCAATGGA	780
	TTTGGCAGCT ATCCTCTCTA CAGCAGTACG CGCTCAGGAC TCAATATGGC TGTTCGGATG	840
	CATGGATTCT GCCCTCAGTA CCGTGGATCG CTTGAGCTGA AAGTCTCCGA GCGATTCCGC	900
	TTTGCCGTCG GTATGGAGCG CGAATACAAT ATCTGGACTC GTCGGTGGGA AACGCATTAC	960
	TTTGCTTATC CTGTATTCTA TGGCGATAAG AAG	993

30

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 744 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15

(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

	ATCAAACGAA TAGAAATGAA AAGGATTTTT ACTGTAGCCC TTGTGCTACT TGCTTCGGTC	60
20	ACTATGGCCA TCGGACAAAG CCGCCCGGCA CTTCGCGTAG ATGCCAACTT CGTAGGCAGC	120
	AATCAGAGCA TGAAAAGAGA CGGATATGTG TGGGACACCA AAATGAATGT CGGCCTGCGG	180
	GTCGGTGCCG CTGCCGAATT CATGATCGGA TCAAGAGGAT TCTACTTGGC TCCGGGTCTG	240
	AACTATACGA TGAAGGGCTC CAAAACCGAA TGGGATATAC CCGAAATGGT TCCTGGTACC	300
	TATATTACGA TGGTTTCCAC TCGCTTGCAC TATCTGCAAC TGCCGATCAA TGCCGGCATG	360
25	CGGTTCGACC TGATGAATGA CATGGCGGTT TCGATCGAAG CGGGTCCTTT CCTTGCATAC	420
	GGTATATATG GTACATATCG GCAGAA GTTG GAAGGATGGA AGCCGAACAA CTACAGCACA	480
	GAGTTTTTTG GCCCAACGCT TGGTGGCCCA ACAAATATCC GCTGGGACAT CGGGGCAAAC	540
	ATAATAGCCG CATTCCACTA TAAGCGTTAT TATATACAGA TAGGCTATGA ACATGGATTT	600
	GTGGATATTG TGTCAGGTGG AGGTTCTGAT ATTCCCCGAC TGAACGACAA TAGGCAATCC	660
30	TCTTCGACGA CCGCTCTAAG AGAAAAGGGA AATAACGAAT ACGCTTATAA TCGTGACTTC	720
	TTCGTGGGCA TAGGTTACCG CTTT	744

(2) INFORMATION FOR SEQ ID NO:27

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

5

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

15

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

20

	TCGCTAATCA ACAATTCAAG AGACTGGAGG GCTCCTGTCC GATTGAGTCT CAAAAAAAAG	60
	ACAAAAACTA TGAAGACAAA AGTTTTACGC AAATTCGTGG TGGCGGCTTT CGCCGTCGCA	120
	ACCCTCTGTC CTCTCGCCCA AGCGCAGACG ATGGGAGGAG ATGATGTCAA GGTGGTCCAG	180
	TACAATCAGG AAAAAGTGGT ACAAACGAGG ATGAGTGTGG CGGACAACGG ATGGATCTAT	240
25	GTAATGACCC ACAGTGGATA CGACACCGGC AATAGCAATG TGAAGATCTT CCGCTCCAAA	300
	GACCAAGGTG CCACATACCA AAAGTTGAGG GATTGGGATC CATCGGATGA TTATCAGTTT	360
	CAAGACTTCG ATATCGTGGT AACGGGTAAG AATGAATCCG ACATCAAGAT TTGGTCGGTA	420
	GAGCTCATGA ATAAGCCCGG AGGATATAAG AGTAGAGTTG CGGTCTTCAG TCGCGATGCC	480
	AACGCGCAGA ATGCGAAACT CGTGTATAAG GAAGACTTCT CCAATGTGCA GTTGTACGAT	540
30	GTGGATATAG CCTCCAATA TCGTTTCGCCT TCTTCTCTTA ACAATGGTGG CAACCCTTTT	600
	GCTTTGGCTT TCGCTTACAC CGGCTTCAAC AATACGCACA AAATAAGTTT TGTGGACTAT	660
	GTGTTCTCTC TGAATGGAGG GCAAAATTTT AATAAAAACT TACTCTTCAG TCAAGATGGA	720
	GAGAAGAAAA TTGACAAGGT GGATCTCTCA TTGGGTAGCA CCTCTGAATC CATGGGTCAC	780
	AATGCCTGGC CGCTAATGGG TGTGGTATTC GAAATGAATA AACAAGGGGG AAAAAGCGAT	840
35	ATCGGTTTCT TGTCGAACTT TGTCGACAAT GATCCCGAAT TTCAGTGGTC AGGCCCTATA	900
	AAAGTGAGTG AAAGCGACAT GTCGTTTCAGC CCCAAAATCC AAATGTTGCT GGACGAGGAT	960

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AACAAATACGA TCAATGGGGA GAGTTGCCAC AACTTCATGA TTACGTACAG CGATTATGAT 1020
TCTGAATATT CGGATTGGGA CATTCGGTAT GTATATCCCA AGAAATCGTT CAAGTATGAA 1080
AAAGGAAAAA CTCCGACTAT GGATGATCTG GTGGAAGCTT TCCTTACAGC TTCGTACCAG 1140
AGTGAGACCA ACTCGGGGCT GGGGTATGAC AAGAACGCCA ATCACTACCT GATTACATAT 1200
5  GCCAAAAAAG AAGAGAACGG TACGAACACG CTGAAATACC GCTGGGCCAA TTATGACAAG 1260
ATTCATAACA AAGATTTGTG GAGCGACACA TTTACGTATA CATCATCTGC CAATGCTCTC 1320
TACACACCTC AAGTAGACAT CAATCCGACC AAGGGTCTCG TGTGCTGGTC ATGGGTGGAA 1380
TATCTGCCGG GCAAACGGAT CGTTTGGTCT GATACGCAGT GGACCCATGC CAACGGTGTA 1440
GAAGACATCG TAATGCAAGA AGGCAGCATG AAGCTCTACC CGAATCCGGC TCAAGAATAT 1500
10 GCTGTGATTA GCCTGCCGAC GGCAGCAAAC TGCAAGGCTG TTGTTTACGA TATGCAGGGC 1560
AGAGTAGTCG CTGAGGCTTC TTTCTCCGGC AACGAATACA GGCTGAACGT GCAGCACTTG 1620
GCTAAGGGTA CGTACATACT CAAGGTCGTA TCCGATACGG AGCGTTTCGT AGAGAAGCTC 1680
ATCGTGGA 1689

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15

(2) INFORMATION FOR SEQ ID NO:28

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1134 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
35 (B) LOCATION 1...1134

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

	GGGATAATAT CTGTTCTTTC ACATGTGGTT GACCGTCCAC AATGGGGTGC TTCTCCCGAA	60
	GCTGCTGGCA CGCATAGTGT GTATTGATT CTACATCCCT CCGCCGGTAT TATCCGGATC	120
5	AGGTCTATGG GTATTATCTC AGCCTGCCGT ATCGCAATTC TTGCCGGCAA GCACCCCGT	180
	AGCGGTCTGT CGAGGGCAAA TGTAAGTATT CTTTCGTACA ATCCAGAAAA CACGCCCGAG	240
	AAAAAGAGAA AACTGCAAGA AAAAAATGTT TTCCTCCAAA TCCGGCTCCG TCAATCATTT	300
	AATAATTTGA TACCTTCGCT CCCATTTAGA ATCGATAACA CAAAAAAAT CACTGAAATG	360
	AAAAAACTA CTTTGACAGG ATCGATATGT GCTTTACTCC TGTTTTTGGG TCTCTCGGCC	420
10	AATGCCCAAT CGAAGTTAAA GATCAAGAGC ATTGAGGCAG CTACCACTTT CAGTTCGGCC	480
	ACGGCCGGAA ATGGTTTTGG TGGCAATATC TTCGGCATGG ACATGAGCAT ACGGATGAGG	540
	GTACACCACA GCATTCTGCC CGAAGGGTTG GATTTTTTCGG TAGGAATACA TGAAAGAAGA	600
	GCACACTGGG AAGAGGCCGG AAGTCCGAAG CTCATGTATA CGAATGTCCC AAGTATCATT	660
	GGTATTGTTG AAAAGGTAAT AGTCTTCGAA GACGCAGAAG ACTTTTTTGA CAAAAAAGCT	720
15	CTCGGCCGCT TCCTCATCAG TTTGGGGATA TCCTATACCA AGCATCTGGG AGCGTATTGG	780
	GGATGGACCA ATGACGCCCA TATTCTTTTC TCACCGATAC CCAAGAGCAA GGTCCACTAT	840
	GACACCTACA CAAGAGCTGG CAGTGACCTT GTACTTCAGT CCGAAGATGT TGCCACAGTG	900
	AGCAATGGCT TTTCACCGGG GATCGGACTC AAAAGTTCTA TTTGGTGGAA AATGCCCATC	960
	AAGAGCAAAT ATGATTTTCG CCTCGGTTTC AGCCTGGGCT ATGAGTATCT GAACCTGCTA	1020
20	TATCCGTATC GTAATTTCAA GCTGGATGGA AATAAGCCGC TTTCAGCACT ATCTCCTCGC	1080
	ATGAACCACA TCGGCCATGT GGGCTTCAAC TTTACCGTGG GTCTTTGGAC TAAT	1134

(2) INFORMATION FOR SEQ ID NO:29

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

10

	ATTTGTGGCA GTAAAATGAA TCTATCGGGA TTACAATCTT TCACTATGAT GAAATCCATG	60
	CGCAGCGTGC TGTGTCTACT CTTTCCATTG TCTTTGATCA CTGCTTTGGG CTGTAGCAAT	120
	AACAAAGCTG CCGAATCGAA GTCTGTCTCT TTCGATTCGG CCTATCTCGA ACGCTACATC	180
	CCTCTGCGGG CAGACATAGA TACGCCATCG CTGCATGTGA TGATCAGCTA CGTCTATCCT	240
15	TCGGGAGATG ATATGCTCAC AGAGATTTTC AACGGTTTGC TCTTCGGCGA CAGCCTGATG	300
	GATTCCTCTT CGCCGGAGAA TGCCATGGAA GGCTATGCAC AGATGCTGGG AGAAGACTAT	360
	CGCTCTAACA ATGCCGAAGC CAATCTGCAA GGGCTTCCTT CTGACCTTTT GGACTATATC	420
	TACAAGCAGG AAAATACCAT CGCTTATTGC GATACGGGAT TGATCTCCAC GCGCATCAAT	480
	ACATATACTT ACGAAGGCGG TGCACATACG GAGAATACAG TCCGGTTTGC CAACATCCTT	540
20	CGCACCAACCG GCAAGGTGCT CGAAGAGCGA GATATATTCA AGATCGACTA TGCGGAAAGG	600
	CTGTCCGCAC TCATCATAGG ACAATTGGTG CACGATTTTCG GCAAGACCAC ACCTGCCGAA	660
	TTGGATGCAA TAGGTTTCTT CAACGCAGAA GAAATACAGC CCAATGGCAA TTTTATGATC	720
	GATGACAAAG GTCTCACATA CTGTTTCAAT GAGTATCAGA TAGCTGCTTA TGCCAGAGGT	780
	GCTGTCTATG TCCGTCTCGG ATATGACGTA TTGGCTCCTT TGCTAAGGGA TGATTCCCCA	840
25	CTAAAGCGTT ACTTGCCG	858

(2) INFORMATION FOR SEQ ID NO:30

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1236 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

35

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

10

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

15	GGAGAGTATC CTGCAAACAG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAAGA	60
	AGTTTGCTCC TGCTTGGAGC GGTACTGCTG ATTACGCTTC CTGCGTACTC GCAGAATGAT	120
	GACATCTTCG AAGATGACAT CTATACATCG CGAAAAGAAA TACGTAAACA AAACCAAGTT	180
	AAAGACTGGC AAAACCAAGA GGACGGATAC GGCGACGATA CGGAATATAC AGTGGCTTCC	240
	GATCGGGACA TTGACGCCTA CAATCGTAGA GATGGCCAGT CCTACGATGG GAAAAAGTTG	300
20	TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTC CCGGTCGCTA TAGTCGCCGC	360
	TTGGCTCGAT TCTATAAGCC GAATACGATC GTCATTTTCA GTGCCGACAA TGTATATGTA	420
	ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA	480
	AACATTTACA TCAACAGTCC TTGGTGCGAT CCGTTCCCTT ATACGTCATG GTATCCATCT	540
	TTCTCCGGCT GGTACAAC TAACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC	600
25	GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC	660
	TACAATCCCT ATGGAATCGG TATGGGTTGG GGATATCCTT ATGGCTGGGG CAGCTATTAC	720
	GGTTGGGGTG GCTATCCGGG AGTGATACAT CACTACCACC ACTACCCCAA GAAGACCTAT	780
	TCCAATGGTC AGCATTCCGG AGCTTACTAT TCTTATGGCC GACCGAATCG TATCAAAGGT	840
	GGAACGTCCG GTGCCAACT TGGGACAGGA CGCTACGATA GAATTCAAAA TTCGTCTTCG	900
30	CAAAAAAATA AGTTCGGATT GCAGTCGAAC AAACCCAATA ATAATCTGCA AAATGTCAAG	960
	TCGGGACGTA CCGGCCGAGC CAATAGAGAC CGAAATATAG AAACGGTAAC TCCAAACAAC	1020
	GGGCAAAAGC AGAATCGTCC CGTATTCCAG CAGAATCAGT CCGGCAATGA CCGACCGACC	1080
	GGACGGAATA TCCGCAGCGA GAGACAGGGG GAAAATAACG ATAGGACATT TTCGACTCCT	1140
	TCTCGTAGCA ATAGTAACGG TGGCTTCTCC ACGCCTTCTC GCTCTTCTTC CGGCTCTATG	1200
35	AGCGGAGGTG GCGGACGTAG TGGCCGGGGA CGCAAT	1236

(2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

25	AAAAGAAAGA GTATGAAAAG AATGCTGCTG CTTCTCGTTG TATTATTATA TGGAATTGCA	60
	GGCCGATTGG CTGCACAAGA CGTTATCAGA CCATGGTCAT TGCAGGTCGG AGCGGGATAC	120
	TCCGATACGG AGAACATCCC GGGAGGATTC ACCTATGGTT TCTATTTGGG AAAGCGTATG	180
	GGGAGCTTTC TGGAAGTGGG GCTGTCCATG TACAACTCCA CACGTCAAAC AGCCAACAAT	240
	GCAGACTCCT TTGCATCGAA CGAAGGAGAC GGATCTTTTC AGGTAAATAT GTCTTCTCCG	300
30	AATGAGAAGT GGTCATTCTT CGATGCAGGC AGTGCCAACT GCTATATGAT CGTCGTCGGA	360
	GTCAATCCTC TCCATCTGTT TTGGCAGAAT AGCCGGCACA ATTTGTTTCT GGCAGTACAA	420
	GCCGGCCTGT CCAATAAGCA CAATATTCAT TTCATCTATG GAGACAAGGG AGCCAAAGTC	480
	AGTATCTACA CCAATTCGAA TACCTACATC GGTACGGAG CACGTGTAGC CTACGAATAT	540
	CAAATTCATA AAAACGTGGG GCGGGGTGCC GCTGTAATGT ACGACCACGG CAATAAGATG	600
35	CTTACGGCCA TGGCCACGCT CTCCACTCAT TTT	633

(2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- 10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION 1...2358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

25 ATCGTTTACC TTTGTCACTG TATGAACCAC AGACGATCAA AAACCATGCT GACGATCCGA 60
AACTTCCTCC TCTTTTGTTG TCTGTCGCTG ATAGCGTTTG CTGCCGATGC ACAAAGCTCT 120
GTCTCTTCGG GTAGACGACT GACAGAATAT GTCAATCCCT TTATCGGAAC GGCCAATTAC 180
GGTACCACGA ATCCGGGAGC AGTATTGCCC AATGGGTGTA TGAGCGTTAC CCCTTTCAAT 240
GTCAGCGGAT CGACAGAGAA TCGCTTCGAC AAAGATTTCG GTTGGTGGAG TGCGCCTTAT 300
30 TCGGCCGACA ATAGTTACTG CATCGGTTTC AGCCATGTGA ATCTGAGTGG AGTAGGCTGT 360
CCCGAACTGA GTGGAATACT GCTGATGGCC ACTTCCGGCA CATTGATCC TGATTACTGC 420
TGCTATGGCT CTTCGCTCAG TCGAGAATAT GCGCGCCCGG GAGAATACAA GGCTGTATTG 480
GACAAATACG GTATAGATGC AGCCGTGACC GTAACCGAGC GGACTGCTTT GACCGAATTT 540
GCTTTTCCCG AAGGAGAAGG CCATATCCTG CTGAACCTGG GACAGGCCCT AAGCAATGAA 600
35 TCGGGAGCCT CTGTTTCGATT CTTAAACGAC TCCACAGTCG TCGGCAGCAG GCTGATGGGG 660
ACGTTCTGCT ACAATCCGCA AGCAGTTTTT CGTCAGTATT TCGTACTTCA GGTGAGTCGG 720

	CGACCGATCT	CTGCCGGCTA	TTGGAAGAAG	CAGCCTCCTA	TGACAGTGGA	AGCCCAATGG	780
	GATTCGACTG	CAGGGAAATA	TAAGCAGTAC	GACGGCTACA	AGCGTGAGAT	GAGCGGTGAT	840
	GACATCGGTG	TCCGATTCTC	GTTCAACTGC	GATCAGGGGG	AAAAGATCTA	TGTACGATCG	900
	GCCGTTTCAT	TCGTCAACGA	AGCCAATGCG	CTCTATAATC	TGGAAGCGGA	GCAAGAAGAG	960
5	GTGTTCAAAA	GTGTCGGAGG	GAATCCGGCC	AAGGCTTTCT	CCGCTATACG	CTCTCGCGCT	1020
	ATAGAGCGTT	GGGAGGAAGC	CCTCGGTACG	GTGGAAGTGG	AAGGAGGCAC	ACCGGATGAA	1080
	AAGACGATAT	TCTATACCGC	ACTCTATCAC	CTGCTGATAC	ATCCGAATAT	CCTACAAGAT	1140
	GCCAATGGAG	AATATCCTAT	GATGGGCAGT	GGCAAAACGG	GTAATACGGC	TCACGACCGC	1200
	TACACCGTGT	TCTCTCTTTG	GGACACGTAC	CGCAATGTAC	ACCCGCTGCT	CTGCCTCCTC	1260
10	TATCCGGAGA	AGCAGTTGGA	TATGGTACGG	AACTGATCG	ACATGTACCG	AGAGAGCGGG	1320
	TGGCTGCCGA	GATGGGAGCT	GTACGGACAG	GAGACCCTGA	CGATGGAGGG	CGACCCCTCG	1380
	CTTATCGTCA	TCAATGACAC	TTGGCAAAGG	GGCCTTCGTG	CTTTCGATAC	GGCAACGGCC	1440
	TATGAAGCCA	TGAAAAAAAA	TGCTTCTTCG	GCAGGAGCGA	CCCATCCGAT	CCGTCCTGAC	1500
	AACGACGACT	ATCTCACCCCT	CGGCTTCGTA	CCGCTTCGCG	AACAGTACGA	CAATTCCGTA	1560
15	TCGCATGCGC	TGGAATACTA	TCTGGCCGAC	TGGAATCTGT	CCCGGTTTGC	CCACGCACTT	1620
	GGGCATAAAG	AAGACGCAGC	TCTATTCCGA	AAACGCTCGT	TGGGCTACAG	AACTATTAT	1680
	AATAAGGAGT	ATGGTATGCT	GTGTCCATTG	CTGCCGGATG	GATCATTCCT	CACTCCTTTC	1740
	GATCCCAAAC	AGGGTGAAAA	CTTCGAGCCT	AATCCCGGTT	TCCACGAGGG	CAGTGCTTAT	1800
	AACTATGCCT	TTTTTCGTTCC	CCACGATATA	CAAGGGCTTG	CCCGGCTGAT	GGGAGGAGCA	1860
20	AAGGTTTTTTT	CGGAAAGGTT	GCAGAAAGTC	TTCGATGAAG	GATATTATGA	TCCGACCAAC	1920
	GAGCCGGACA	TCGCCTATCC	TTACCTCTTC	TCCTATTTCC	CCAAGGAAGC	ATGGCGAACG	1980
	CAGAAATTGA	CCCGGGAGTT	GATAGACAAA	CATTTTTGCA	ATGCTCCTAA	CGGCTTGCCC	2040
	GGTAATGACG	ATGCCGGTAC	GATGAGTGCT	TGGCTTGTCT	ATTCCATGCT	GGGATTCTAC	2100
	CCTGACTGTC	CGGGCAGCCC	CACCTATACA	CTGACCTCGC	CGGTATTCCC	CCGAGTTAGG	2160
25	ATTCCGGCTCA	ATCCGCAGTA	TTATCCTCAG	GGGGAGTTGA	TCATTACGAC	CAATACAGAG	2220
	AATCAACCGA	CAGATTCCAT	TTACATCCAT	ACGGTTTCTC	TTGGCAATAA	AACACTTCCG	2280
	CATGGAACAA	GGCATATCAG	CCATGCCGAT	TTGGTGCGCT	GCGGTCACCT	CCGTTACGAA	2340
	CTAAGCAATC	GTCCTCGA					2358

30

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2859 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2859

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

	ATCCGAATGA GAGTATCCGA TCTCTGTTCC AGACTTTCAT GGTTATTACC CGTAATCCTT	60
	GTCGGATTGC TCTGTGCTAC TTTGGTCGCT GCGGAACGTC CTATGGCCGG AGCAGTCGGA	120
20	TTGCACCACC GTCGGCATGC TGCGCTGTCT GATTCTACAG CGAAAGACAC GGTGCCTCTC	180
	GCAAAACCTA TTCCTGACAG TGCTTTTCGA GATTCCCTTC CTGCCGATTC CACCGGATCG	240
	ATGCGGCAAG ATAGCGTGTA TGACGATGAA TTCGAATTGG AAGATATAGT GGAGTACGAA	300
	GCTGCCGATT CCATCGTTTT GCTCGGACAG AATCGTGCCT ATCTTTTCGG CAAGAGCTAT	360
	GTGAGCTATC AAAAGAGTCG CTTGGAGGCA AACTTCATGT ATCTCAATAC CGACAGCAGT	420
25	ACGGTTTATA CTCGCTATGT CCTCGATACG GCCGGTTATC CGATGGCCTT TCCTGTTTTT	480
	AAGGATGGAG AGCAGTCGTT CGAAGCCAAG AACTTTACCT ACAACTTCCG CACGGAGAAG	540
	GGGATTATCA GCGGAGTGAT CACGCAGCAG GGCGAAGGCT ATCTGACTGC CGGTAAGACC	600
	AAGAAGATGC CCGACAATAT CATGTTTATG CAAGGAGGGC GTTATACGAC CTGCGACAAT	660
	CACGATCATC CTCACTTCTA TATCAATCTT TCCAAGGCAA AGGTGCATCC GGAGAAAGAC	720
30	ATCGTCACAG GTCCGGTCAA TCTGGTTATC GCCGATATGC CGCTGCCGAT AGGTCTTCCT	780
	TTCGGCTATT TTCCCTTTTC CAACAAATAC TCTTCCGGTA TATTGATGCC CACGTACGGA	840
	GAGGACAATC GCTATGGATT TTATTTGAGG AATGGTGGAT ATTATTTTGC CTTACGCGAC	900
	TATATCGATT TGGCATTGCG TGGGGAGATC TTTTCCAAAG GGTCATGGGG CATTTACGCC	960
	CAATCGAAAT ATAAGAAGAG GTATAAGTAC AACGGCTCGT TCGAAGCCAA TTATCTGGTA	1020
35	TCGAAGTCCG GCGACAAATA CGTGCCCGGA GACTACAGCA AGACCACCAG TCTGAATATC	1080
	CGATGGACAC ACAGTCAGGA TCCGAAGGCC AATCCTTTGC AAACGTTGTC GGCCAATGTC	1140

	AATTTTGCCA	CCGGGAGCTA	TTTCCAGAAT	TCGCTGAATA	CCACCTATGA	TGTCAATGCC	1200
	CGTACTGCTA	CGACACGAAG	TTCGGCCGTG	AGCTATTTCG	GCAAGTTTCC	GGGTACTCCT	1260
	TTTTTCGATTA	CGGGTAGCAT	GGATATCAGC	CAGAACATGC	GCGATACGAC	GGTGAGCCTT	1320
	ACCTTGCCGA	ATCTTTTCGAT	TAATATGTCC	ACGCGTTATC	CTTTCAAGCG	GAAGACCCGT	1380
5	GTAGGACCGG	AGCGATGGTA	CGAGAAGTTG	AGTGTGGGCT	ATTCCGGTCA	GCTTCGCAAT	1440
	AGTATCTTGA	CAAAAGAGAA	AGATTTGCTC	CAGAGCAATC	TCGTGCGCGA	TTGGAAGAAT	1500
	GGTATGCGTC	ATTCCGTACC	GATCAGTTTG	ACTGTCCCTT	TGTTGGATTA	TATCAATCTG	1560
	ACTATGGGGG	TTAACTACAA	TGAGTGGTGG	TACACGAAAG	GCATACGGAA	GTCGTGGAAT	1620
	GAGGATAAGA	AAACATTTCCT	GCCTTCGGAC	ACGACCTATA	AATTCCGCAG	ACTGTACGAT	1680
10	TACAGTCTGT	CGGCAGGCTT	ATCTACCACA	TTGTACGGTA	TGTTCAAGCC	TTGGAAACCT	1740
	TTTTCTTCG	GAGGCAATCT	CATTATGATC	CGTCATCGCT	TCACGCCCAC	TGTCAGTTTC	1800
	TCCTATATGC	CGGACTTCAC	GAAACGCCGA	TATGGCTTTT	GGGAGCTTCT	TGAGCATACG	1860
	GATCAGAACG	GCAAGCTGCA	TACGCTGCTC	TACTCTCCTT	ATTTTCGAGCA	GATATTCGGT	1920
	GCTCCCTCCA	TGGGCAATGC	AGGATCTGTC	AATTTCTCTT	TTGACAACAA	CTTAGAGGCC	1980
15	AAGATCAAAT	CCAAATCGGA	TTTCGACAGG	ATCAAGAAGA	TCAGCCTGAT	AGATCAGTTC	2040
	ACATGGTCTA	CATCCTATAA	TATGTTTGCC	GATTCGATCC	GATGGAGCAA	TATCTCGGCT	2100
	TCGCTGGCAC	TTCGCCTCTC	CAAGAGCTTT	ACCTTGCGCT	TGTCCGGTCT	GTTCGATCCC	2160
	TATTTGACGA	AGTATTATGA	GGGAGAAGAT	GGGAAGATCA	TTCCCTATAA	GAGCAACGAC	2220
	CTGCGCATTT	TTAACGGCAA	GGGATTGGCA	CGCCTGATCA	GTACGGGTAC	TTCTTTTCAGC	2280
20	TATACGCTCA	ACAAAGAGTC	GCTCAGCGGA	TTGATAGCTC	TTTTTCAGTGG	CAAAAAGGAG	2340
	CGGAGAGATG	AAAAGAAAAA	CACAGGGGCT	ACTCCTCATG	AAGGAGACGA	TGCTGCCGAT	2400
	ATACTTGAGG	GAGGAAGACC	GCAAAATGAA	AGTGGGGGGT	CGCTCCTCGA	GCGCAACCGT	2460
	CAGGGCGGAG	CAGTGGATCA	GGATGGTTAC	TTCGCATATT	CGATCCCATG	GAGCCTGTCC	2520
	TTTCGACTATA	GTTGGAATAT	TGCTACCGAC	TACAATAGGT	ACAATGTCAA	TAAGATGGAG	2580
25	CACTACTACC	GGGTAACGCA	GAATCTGAGC	TTTCGCGGCA	ATATCCAGCC	TACACCGAAC	2640
	TGGAGCTTCG	GATTCAATGC	GAACTACAAT	TTCGACTTGA	AGAAAATAAC	ATCGCTTACC	2700
	TGCAACGTCA	CTCGCGACAT	GCACTGCTGG	GCTATCTCGG	CCAGTTTCAT	CCCTATAGGA	2760
	GCATACAAGT	CCTATAATTT	CGTCATATCG	GTGAAGAGTT	CACTCTTGCA	GGATCTGAAG	2820
	TATCAGCAGA	GCAATCGTCC	CATCACGAAT	ACTTGGTAT			2859
30							

(2) INFORMATION FOR SEQ ID NO:34

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1803 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15

(B) LOCATION 1...1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

	AGTAATAGCA GCTCCACAA GTGGTTAATT TATTATCATA TAGAAAAGAC TAAAAGTATT	60
20	ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG	120
	GTACCAACGG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC	180
	TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT	240
	CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC	300
	TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCCTT- CGAGGATCTC	360
25	TATAAGCCCC TGCCCGGACA TGAACCCGAG ATGNGGCGTG GCGTTCCTCA CATGTATGTG	420
	AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC	480
	GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC	540
	GGACGTATAG TACTCACTCC TTTTGATGGA GTGCGTGTCA AGGGTATTGC AGGACAGCAG	600
	CGTAACTACT TCGACCGCAC GGGCAAGGTA TTCAATTCCG GCCGAGGCTA CCTACTGGGT	660
30	TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGCGCGACAA TGAATATCAT	720
	TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT	780
	GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC	840
	ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT	900
	CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCTCA	960
35	TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCTTTC	1020
	CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC	1080

	CAAGCTCACA	CTTATACGCT	GGCGGCCATC	TACCCCTATG	CTACTCAGCC	TCAGGGAGAA	1140
	TGGGCTTTCC	AAGGTGAACT	GCGTTACAAC	TTTGCTCGCC	GGACAGCTCT	CGGTGGACGC	1200
	TACGGTACCG	GCTTGCGTAT	CAACGTTTCG	CATGTGCGTG	GTCTGGACAA	AAAGATGCTC	1260
	AAAGAGAATC	CCGACGAACT	GATCGGAACG	GATGGCTACA	CCGTTTCTTT	CTTCGGCATG	1320
5	GGCGACCTCT	ATTATTCGGA	TATAGATGTG	GAGATTACTA	AAAAGGTAAG	CCCAGGATTC	1380
	AACTTTACGC	TCACCTACTT	GAATCAGATC	TACAATAACA	AGGTACTGCA	CGGTGCAGCC	1440
	GGAGAGAAGC	CTGAGAAGAT	CTATGCCAAT	ATCTTCGTCT	ATGATGGTAA	GTATAAGCTG	1500
	AGTAATAAGG	TAGCCCTCCG	TACCGAACTG	CAATATTTGC	ACACGAAGCA	GGATCAGGGT	1560
	GACTGGATCT	ACGGCATGGC	CGAGCTCTCT	ATCCTGCCTT	CTCTGATGCT	TTCCCTCTCG	1620
10	GAGCAGTATA	ATATCGGAGA	GACCAAGAAA	CATTATGTCA	TGGGGTCTGT	CACCTATACT	1680
	CACGGAGCAC	ATCGAGTAGC	TTTCTCTGCA	GGCAAACCC	GTGCAGGGAT	GAAGTGCTCG	1740
	GGAGGTGTAT	GTCGTGTGGT	CCCTGAGACT	CAGGGATTCT	ACCTTTCTTA	TAGCACCAAT	1800
	CTG						1803

15

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|-----------------------------|
| | (A) LENGTH: 2886 base pairs |
| 20 | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: circular |

(ii) MOLECULE TYPE: DNA (genomic)

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- | | |
|----|----------------------------|
| | (A) NAME/KEY: misc_feature |
| 35 | (B) LOCATION 1...2886 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

	GCCATTTTTG TCGTATCATT GCAAATTGAA AAAATAACAG AGAATAAGTA TAATTCAGAC	60
	AAGAGCATGA ACAAATTTTA CAAATCACTT TTGCAGTCAG GACTGGCTGC CTTCGTGTCG	120
5	ATGGCAACTG CACTGACCGC TTCTGCACAG ATTTCTGTTTCG GAGGGGAACC CTTGAGTTTC	180
	TCTTCAAGAT CCGCCGGAAC GCATTCATTG GACGATGCAA TGAATATCCG CCTTACTCCG	240
	GATTTCAATC CGGAAGACCT GATCGCACAG AGCCGTTGGC AATCGCAAAG AGATGGCCGG	300
	CCCGTCCGGA TAGGACAAGT AATACCGGTG GATGTGGACT TTGCATCCAA GGCTTCGCAC	360
	ATCTCTTCCA TCGGAGACGT AGATGTATAT CGCCTGCAAT TCAAGTTGGA AGGAGCCAAA	420
10	GCCATTACGC TTTATTACGA TGCATTCAAT ATTCGGGAGG GCGGACGCCT CTATATCTAT	480
	ACCCCCGACC ATGAAATTGT GTTGGGAGCA TATACGAACG CCACTCATCG CCGCAACGGA	540
	GCTTTTGCCA CAGAGCCGGT ACCGGGGAGT GAGCTTATTA TGGATTATGA AGTGTCTCGC	600
	GGAGGGACTT TGCCTGACAT CAAGATCTCC GGTGCGGGTT ATATATTCTGA CAAAGTCGGC	660
	GGACGCCCCG TAACGGATAA CCATTACGGG ATCGGTGAGG ACGATTCCGA TTCGGATTGC	720
15	GAGATCAACA TCAATTGTCC TGAAGGTGCA GACTGGCAGG CAGAGAAGAA CCGTGTGGTG	780
	CAAAATGATCA TGGTAAAAGG ACAGTATATC TCAATGTGCT CAGGCAACCT GCTCAATAAT	840
	ACGAAAGGAG ACTTTACTCC GCTGATCATT TCTGCCGGAC ACTGTGCTTC CATAACAACC	900
	AATTTCCGTG TAACGCAATC CGAGTTGGAT AAGTGGATCT TCACTTTCCA CTATGAAAAA	960
	AGAGGATGCA GCAATGGTAC ATTGGCCATC TTCCGTGGCA ACAGTATCAT CGGAGCTTCC	1020
20	ATGAAGGCTT TCCTCCCGAT CAAAGGTAAA TCCGATGGTC TCTTGCTGCA ACTCAACGAT	1080
	GAAGTCCCTC TGCGCTATCG TGTCTATTAC AATGGATGGG ACAGTACGCC CGATATTCCC	1140
	TCGAGCGGTG CCGGTATTCA TCATCCGGCC GGAGATGCCA TGAAGATTTC CATCCTAAAG	1200
	AAGACTCCGG CTCTGAATAC ATGGATCTCC TCCAGTGGTT CCGGAGGGAC TGACGATCAC	1260
	TTCTATTTCA AATACGATCA AGGTGGTACG GAAGGAGGAT CGTCCGGTTC TTCTCTCTTC	1320
25	AATCAGAATA AGCACGTGGT CGGCACACTG ACCGGAGGTG CCGGCAATTG TGGCGGGACG	1380
	GAGTTCTACG GCAGACTGAA CAGTCATTGG AACGAGTATG CATCCGATGG CAATACGAGC	1440
	CGCATGGACA TCTATCTGGA TCCCCAAAAC AATGGCCAGA CGACCATCCT CAACGGAACG	1500
	TATCGTGACG GTTATAAGCC TTTGCCCTCT GTGCCCCGGC TATTGTTGCA GTCTACAGGC	1560
	GATCAGGTCTG AATTGAATTG GACGGCTGTT CCTGCCGATC AATATCCATC ATCTTATCAG	1620
30	GTCGAATACC ACATATTCCG AAATGGAAAG GAAATAGCTA CGACAAAGGA GTTGTCTTAT	1680
	TCGGATGCCA TCGACGAAAG TATTATCGGT AGCGGTATCA TTCGATACGA AGTAAGCGCA	1740
	CGCTTCATTT ATCCCTCGCC GTTGGATGGA GTGGAATCTT ATAAGGATAC GGACAAGACT	1800
	TCTGCCGACC TTGCCATAGG AGACATTGAG ACCAAGCTGA AGCCGGACGT AACACCTCTC	1860
	CCCGGAGGAG GAGTATCATT AAGCTGGAAA GTTCCTTTCT TAAGCCAGTT GGTTCCTCGA	1920
35	TTCGGAGAAA GCCCCAATCC TGTGTTCAAA ACCTTTGAAG TGCCCTATGT TTCTGCCGCA	1980
	GCCGCACAAA CCCCCAATCC TCCCGTTGGC GTAGTCATTG CAGACAAGTT TATGGCCGGT	2040

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ACATATCCCG AAAAGGCTGC TATCGCTGCC GTTTATGTAA TGCCATCCGC TCCGGACTCT      2100
ACTTTCCACC TCTTCCTCAA GAGCAACACA AACAGAAGAT TGCAGAAGGT GACAACTCCC      2160
TCCGATTGGC AGGCCGGAAC ATGGTTGAGG ATCAATTTGG ATAAGCCGTT CCCGGTGAAT      2220
AATGACCATA TGCTTTTTGC CGGTATCAGA ATGCCTAATA AGTACAAGCT CAATCGTGCT      2280
5  ATCCGTTATG TAAGAAATCC GGATAACCTT TTCTCCATTA CCGGTAAGAA GATTTCATAT      2340
   AACACGGAG TCTCTTTCGA AGGCTACGGA ATACCCTCGC TCTTGGGCTA TATGGCTATC      2400
   AAATATCTGG TGGTAAATAC CGATGCTCCG AAGATCGATA TGTGCTTGT ACAGGAGCCT      2460
   TATGCTAAGG GAACGAATGT GGCTCCATTC CCCGAATTGG TCGGCATATA TGTCTATAAG      2520
   AACGGAACAT TTATCGGCAC ACAGGATCCA TCCGTCACAA CTTATTCGGT TTCAGACGGA      2580
10 ACAGAGAGCG ATGAATACGA AATAAACTG GTATATAAGG GATCGGGCAT TTCGAATGGC      2640
   GTTGCTCAGA TTGAGAATAA CAATGCTGTC GTTGCATATC CGTCTGTTGT AACAGATCGT      2700
   TTCAGCATT AAGAACGCTCA TATGGTTCAC GCTGCCGCCC TCTACTCATT GGATGGCAAG      2760
   CAGGTTCGTT CTTGGAACAA CCTCCGCAAT GGCCTGACAT TCAGTGTTCA AGGACTTACG      2820
   GCCGGTACTT ATATGCTCGT TATGCAGACG GCAAACGGCC CTGTGAGCCA AAAGATCGTG      2880
15 AAGCAG                                         2886

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(2) INFORMATION FOR SEQ ID NO:36

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20      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 3936 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: circular

25      (ii) MOLECULE TYPE: DNA (genomic)

          (iii) HYPOTHETICAL: NO

30      (iv) ANTI-SENSE: NO

          (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Porphyromonas gingivalis

35      (ix) FEATURE:
          (A) NAME/KEY: misc_feature

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(B) LOCATION 1...3936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

5	AAGAGGGTAG ATAGCTATGA ATGCAGACAA AAAGCTTGCA AATGTGCAAT TTGTGTGATA	60
	CAAAAATTTA CTAATGTAAA ACTAAATGAT ATGCGAAAAA TTTTGAGCTT TTTGATGATG	120
	TGCTCTCTGC ATTTAGGTCT ACAATCTCAG ACTTGGCATG GAGATCCGGA CTCAGTGGCA	180
	GCCCTACCTT CTATCGGTAT TCAAGAGTCA AGTTGTACCC GAATCACGTT CGAGGTTGTT	240
	TTCCCCGGAT TTTATAGTGT GGAAAAACGA GAAGGCAACC AAGTCTTTCA GCGCATTTCC	300
10	ATGCCGGGTT GTGGCTCGTT TGGGAATCTG GGCGAAGCTG AATTGCCTGT TTTGAAAAAG	360
	ATGATAGCCG TTCCGGAATT TTCAACAGCT AACGTTGCTG TAAAAATCAA AGAGACGGAG	420
	ACATTCGACA ATTATAATAT CTATCCTAAT CCTACCTATG TCGTAGAGGA GTTGCCTGAG	480
	GGGGGGACTT ATCTGGTAGA GGCTTTCGCG ATAAACAATG ACTATTATAG CCAAATGTA	540
	AGCCTCCCTT CTACTCACTA TGTCTATTCT CAAGACGGGT ATTTTCGCTC ACAAAGATTT	600
15	ATCGAAGTTA CCCTGTATCC TTTTCGATAC AACCTGTCC GACAAGAAAT TCTATTTGCA	660
	AAAAAATCG AGGTTACAAT AACTTTCGAT AATCCTCAGC CACCTTTACA AAAAAACACC	720
	GGCATATTTA ACAAAGTAGC CTCCTCTGCA TTTATTAATT ATGAAGCTGA TGGCAAATCG	780
	GCGATAGAAA ATGATATGGT GTTCAGTCGT GGTACAACAA CGTACATAAG CGGAAATGTT	840
	GCCAGCAACC TCCCTCAGAA CTGTGACTAC TTGGTTATTT ACGATGATAT GTTCAACGTA	900
20	AATCAACAAC CACACGACGA AATCAAACGG CTGTGCGAAC ATAGAGCCTT CTACAACGGC	960
	TTTGATGTAG CTGCTGTAAG TATAAAGGAC GTATTGAATA GCTTCCCATC AAATGCCACC	1020
	TCATACATCA ACGAAACTAA ACTGAAAAAT TTCATTGCTC CAGTTTACAA CCAAAGCAAT	1080
	GCGAAGAGGA CTTTAGATGG CAAACTGGGA TACGTGCTAC TGATCGGAAA ACCATTGAGC	1140
	AAATATTTGG CTGACACTGA TAATACAAAA GTCCCAACCT CTTTTATTCA TAATGTCTCC	1200
25	TTAATTCCAA GTCATCCAAC TTTTGGTTCC ATATGCGCCT CCGACTATTT TTTTAGTTGT	1260
	GTTTCGCCCC TTGATACTGT CGGCGATTTG TTTATCGGTC GATTTAGCGT CACCAATGCT	1320
	CATGAATTGC ACAATCTGAT TGAAAAGACT ATCAACAAAG AAATCTCATA TAATCCTATT	1380
	GCACACAAAA ATATTCTTTA CGCAGAAGGG AAAGGCTGCG ATGCTCCAAT CTTACGTTTA	1440
	TTCTTAAAAG AAATCGCCTC TGGTTACACA GTCAACTCTA TCTTAAAATC TAATCAGGTC	1500
30	TCTGCAATAG ACTCGATATT TGAAGTCTTG AATAATGGTT CCCATCATTT TTATTTTAAC	1560
	ACTCATGGAA TGCCGACTGT TTGGGGGATA GGGCAGGGAC TCGACGTCAA TACTCTAACA	1620
	GCCCCGATTGA ACAATACATC TTCGCAGGGA TTATGTACGA GTCTATCATG TAGTTCGGCT	1680
	GTAGCAGATT CAACTATTAG ATCGCTTGGA GAAGTCCTGA CCACATACGC ACCTAACAAG	1740
	GGATTCTCGG CTTTCTTAGG AGGAAGCAGA GCCACCCAAT ATGCCGTTTA TTTAGAAGGC	1800
35	CCCTGTCCTC CGTCAGAATT TTATGAATAT TTACCTTATT CTTTATATCA CAATCTCTCG	1860
	ACTGTTGTTG GCGAAATGTT GCTATCATCC ATTATCAATA CTAATTCTGT TGATACGTAT	1920

	TCGAAATTCA	ACTTCAATTT	GCTTGGCGAC	CCTGCACTAA	ACATTATGGC	TCATGGCATG	1980
	GAGGTTAGTA	ATTGTATTAC	ACTACCAAAC	AACACCATTA	TAAGCAGTCC	GATAACAATA	2040
	AAAAATGGTG	GCTGCCTAAA	AATACCGGAA	AAAGGAGTTT	TGCATTTTAC	TAATAATGGC	2100
	TCCATACAAG	TCATGTCCGG	AGGAACTCTG	GAAATAGGCA	ATCAGGCTAA	AATATCCGGA	2160
5	GAGACCGGTG	CTAACCCAC	CTTTATTACC	GTTTACGGCG	ATGGTCTTGC	GATTAACAAG	2220
	CAGGTAGAGA	TAGACAATAT	AGACCGACTT	AACTTGTTTT	CTACGCATTC	GGTCATGCCC	2280
	AAATTTTCATT	TTGACAGTGT	GAAATTCAAC	AGTGCCCCGC	TGTATACAAC	GAAGTGTATT	2340
	GTGGAGATAA	GCAATTGCGA	ATTTACCAAT	CGAAGTGACA	TTATTTCAAA	GAATTGTGAC	2400
	CTAAGCGTTG	AAAACAGTAT	GTTTAGCAGT	TCGGGGATAA	CGGTATTCAA	GCCTATGGCT	2460
10	ACAAGCTCCA	TCACCGGATT	ATCTACAAAA	GCAAAGATTA	CCGACAATAC	TTTTTTTGCG	2520
	ACAGGAAACT	TCGCCTACCA	TATCACAAC	ACGCCAGGCT	TAACAGCAAC	CTCCAATGCT	2580
	GCCATCAAGT	TAGACAATAT	TCCTGAGTAT	TACATTTCCG	GTAATAAAAT	AGTCAATTGC	2640
	GATGAGGCTC	TTGTACTAAA	TAATAGTGGC	AACAGAACGA	ACAGACTCCA	CAATATCACA	2700
	CGGAATGTGA	TAAAAAACTG	TAGGATTGGG	AGCACGCTTT	ATAATTCCTA	TGGTATTTAC	2760
15	AACCGAAATA	AGATCAGTAA	CAATCATATA	GGAGTACGTC	TCCTCAACAA	CAGTTGTTTT	2820
	TATTTGATA	ATGCTCCTGT	AATCAATGAA	GAAGATAAGC	AGACGTTTAT	TTCTAATAGG	2880
	ACTTGGCAGC	TCTATTCATC	AAACGGTACA	TTCCCTCTCA	ACTTCCATTA	CAACAGCTTG	2940
	CAGGGGGGAG	ATACAGATAC	ATGGATTTAC	AACGACACGT	ATACGAATCG	CTATATTGAC	3000
	GTTTCAAATA	ATCACTGGGG	CAACAATGAT	TTGTTTGATC	CGAATCAGGT	TTTCAATACG	3060
20	CCAGACTTGT	TCATTTGGAT	ACCTTTTTTG	GATGGATTGC	CAAATGGGAG	ATCGGGCAAT	3120
	AGCTCTGCTG	AAGCAGTAGA	ATTCCAAACA	GCATTGGACT	GTATTGGCAA	TAGCGATTAT	3180
	CTTTTCGGCAA	AAGTGGCTCT	CAAGATGATG	GTTGAAACCT	ACCCGGAATC	CGACTTTGCA	3240
	ATAGCTGCTT	TGAAGGAATT	GTTTCAGGATA	GAGAAAAATGT	CAGGCAACGA	TTACGAAGGC	3300
	TTGAAAGATT	ATTTTCAGATC	CAATCCAACC	ATCATCTCTT	CCCAGAACTT	GTTCCCGACA	3360
25	GCTGATTTCC	TGTCTGCGCG	ATGCGATATT	GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	3420
	TGGTACGAAA	ATCGCTTGAA	TAGTGAAATC	TCCTATCAGG	ACAGTGTTTT	TGCAGTCATT	3480
	GACCTTGGTG	ACATTTATTG	GAATATGCAG	TTAGACTCAC	TCAGAGGGAC	TGGTATAGAT	3540
	TTGAACATAC	TTTCCTGTGA	ACAAAGGAAA	TCGCTCGAAA	GCCATCAAAA	TGTAAAAAAT	3600
	TATTTGTTGT	CAACTCTTCC	CGAATCAACA	GGTACTCTCC	TGCCTCCATT	AGAATGCAAC	3660
30	AAATCAAGCC	TTGATAAATC	CAAGATAATC	TCTATTTTCGC	CCAATCCGGC	GAAAGCTGTT	3720
	GTAACAATAA	TCTACTATAC	CGATAACCCT	TCCTGTTCTG	TAATAAAAAAT	ATATGGAATA	3780
	AATGGAGCCT	CGGCTGATAT	AACCGGGTTG	CCCAAACATC	TATCCGAAGG	TTATTACAGC	3840
	ATACAGTTCA	ATACATCCAA	CTTTGATCCC	GGTTTCTACC	TGGTAACGCT	AAATGTTGAT	3900
	CAGAAAATTA	TAGATACGGA	AAAATTACGA	ATCAAA			3936

(2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2814 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

	TCAGAAAATT ATAGATACGG AAAAATTACG AATCAAATAA TGGCTATCAT- GATGAAAAGT	60
25	ATTGTTTTTA GAGCATTCTT AACGATTTTG CTCTCGTGGG CAGCGATCAC GAATCCGACT	120
	GCTCAAGAGA TCTCAGGCAT GAATGCATCC TGTCTGGCTG CTCCGGCTCA ACCGGATACT	180
	ATCTTATATG AAAGTTTGA GAATGGACCT GTTCCCAATG GCTGGCTTGA GATAGATGCT	240
	GATGCTGATG GTGCCACTTG GGGAAGCCCA TCAGGCTCTT TCTCTGTACC TTACGGACAC	300
	AATGGCCTTT GCACCTACTC CCATATACGT TCCGGTATCT CAACAGCGGG CAACTATCTG	360
30	ATTACACCCA ATATAGAAGG AGCCAAACGG GTCAAGTACT GGGTATGCAA TCAGTATAGT	420
	ACCAATCCGG AACATTACGC AGTAATGGTA TCGACAACGG GGACTGCCAT TGAAGACTTT	480
	GTTTTGTTGT TTGATGATTC CATAACAGGG AAACCGACTC CTCTTGTATG GCGTAGACGA	540
	ATCGTGGACT TACCGGAAGG GACCAAATAT ATTGCATGGC GACATTACAA AGTCACCGAC	600
	TCACACACAG AATTCTTGAA ATTGGATGAT GTCAGTGTGT ATAGGTCGAT CGAAGGGCCC	660
35	GAACCTGCTA CCGACTTCAC AGTAATCAAT ATGGGTCAGA ATGTGGGACG ATTGACTTGG	720
	AACTATCCGG AGGATTATCA ACCGGAAGGA AAGGGGAATG AAGAGTTGCA GCTTAGCGGC	780

	TACAACATCT	ATGCGAACGG	TACACTACTG	GCACAAATAA	AAGATGTCTC	CATACTGGAG	840
	TATGTGGACA	GCACTTACTC	TTTGCGAGAC	AATCCCTTGC	AAGTGGAGTA	CTGCGTTACA	900
	GCCGTTTACG	ATGAAAGCAT	AGAATCTTCG	ACCGTATGTG	GCACGCTGCA	TTACGCCACG	960
	GATGCCATCC	TTTATGAAAA	TTTTGAGAAT	GGACCTGTTC	CCAATGGTTG	GCTTGTGATA	1020
5	GACGCTGATG	GAGATGGATT	TAGCTGGGGA	CACTATTTGA	ATGCATACGA	CGCTTTTCCC	1080
	GGCCATAATG	GAGGCCATTG	CTCCTTGTCT	GCTTCTTATG	TTCCGGGTAT	AGGCCCGGTG	1140
	ACTCCCGACA	ACTATCTGAT	TACCCCCAAG	GTTGAAGGAG	CCAAACGTGT	CAAGTACTGG	1200
	GTAAGCACGC	AGGATGCCAA	TTGGGCAGCG	GAACATTACG	CGGTGATGGC	TTCGACAACG	1260
	GGGACTGCTG	TCGGAGATTT	CGTCATATTG	TTCGAAGAAA	CCATGACAGC	GAAGCCGACC	1320
10	GGCGCATGGT	ATGAAAGAAC	CATCAACTTA	CCTGAAGGGA	CTAAATACAT	CGCATGGCGG	1380
	CATTACAAC	GTACCGATAT	ATATTTCTTG	AAGTTGGACG	ATATCACTGT	ATTCCGGGACT	1440
	CCTGCATCAG	AGCCCGAACC	TGTTACCGAT	TTCGTTGTCT	CGCTTATTGA	AAACAACAAG	1500
	GGACGATTAA	AGTGGGAATTA	TCCTAACGGC	TACGAACCCG	ATAAGACTGA	TGATAAAGAC	1560
	CCATTGCAGC	TTGCCGGCTA	CAATATCTAT	GCAAACGGCT	CGCTCCTTGT	TCACATACAA	1620
15	GACCCGACTG	TTTTGGAGTA	TATCGATGAG	ACTTATTCTT	CACGAGACGA	TCAGGTGGAA	1680
	GTGGAATATT	GTGTCACTGC	CGTTTATAAC	GACAATATCG	AGTCCCAATC	GGTTTGCAT	1740
	AAGCTGATTT	ATGATTCTCA	ATCGGACATT	ATCTTATATG	AAGGCTTTGA	GGCCGGAAGT	1800
	ATTCTGAAG	GCTGGTTGTT	GATTGATGCT	GATGGCGACA	ATGTTAATTG	GGACTATTAT	1860
	CCTTGGACTA	TGTATGGACA	TGACAGTGAG	AAGTGTATTG	CATCCCCTTC	GTACTTACCG	1920
20	ATGATTGGCG	TTTTAACTCC	GGATAACTAT	TTGGTTACAC	CCAGACTCGA	AGGAGCCAAG	1980
	CTTGTCAAGT	ATTGGGTAAAG	TGCGCAAGAT	GCTGTTTATT	CGGCTGAGCA	TTATGCTGTG	2040
	ATGGTTTCTA	CTACGGGAAC	TGCTGTTGAA	GATTTTGTCC	TCTTGTTCTGA	AGAGACAATG	2100
	ACCGCTAAGG	CTAACGGTGC	ATGGTATGAG	CGAACTATTA	CATTGCCTGC	AGGAACAAAA	2160
	TATATTGCCT	GGCGGCATTA	TGATTGCACC	GATATGTTTT	TCTTGCTCTT	GGATGACATT	2220
25	ACGGTTTATC	GTTCTACTGA	GACTGTTCCC	GAGCCTGTTA	CTGATTTCGT	TGTCTCGCTT	2280
	ATTGAGAATA	ACAAGGGTCG	CCTGAAATGG	AATTATCCTA	ACGGCTACGA	ACCCGATAAG	2340
	ACTGATGATA	AAAAACCAT	GCAGCTTACC	GGCTACAACA	TCTATGCAAA	TGGCTCGCTC	2400
	CTTGTTTACA	TACAAGACCC	GACTGTTTTG	GAGTATATCG	ATGAGACTTA	TTCTTCACGA	2460
	GACGGTCAGG	TGGAAATGGA	ATATTGTGTC	ACTGCCGTTT	ATAACGACAA	TATCGAGTCC	2520
30	CAATCGGTTT	GCGATAAGCT	GAACATATACT	ATCACATCCT	TGGATAATAT	TCAATCTGAT	2580
	ACAAGCTTGA	AAATATATCC	TAATCCGGCA	TCGTATGTGG	TAAGGATAGA	GGGATTGAGT	2640
	CGGAGCAAGT	CGACAATCGA	GTTGTATAAT	GCGCTGGGAA	TTTGCAATAT	AAGGGAAGAG	2700
	ACTCATTCAG	AGAAAACGGA	AATCGATGTT	TCACGCTTCA	ATGACGGAGT	CTACTTGATT	2760
	AAAGTAGTCG	GTGGAAATAA	AACAACAACC	GAAAAGGTAG	AGATAAAGAG	GCCG	2814

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 3753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...3753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

	AAATGGAAAT TGGCATGCGC TTTTGATTGC GCGTGTTGTT TCGATCCATT TGTAGTAACT	60
25	AACGAGGTAA TAATAATGAT GAAACGATAT ACAATAATTC TTGCAGTTTT TCTTTTATTC	120
	TGCACGGTAT TTACCTTTCA AATAAAAGCT CGCCCTTATG AAAGATTTCG AGATGTAGAG	180
	AAGCCTTGGA TTCAGAAACA TTCAATGGAT TCTAAATTGG TGCCTGCAAA TAAGGGTAAC	240
	TTAATTCAAG CTGAAATTGT ATACCAATCT GTTTCTGAAC ATAGTGACTT AGTTATTTCA	300
	CCTGTGAACG AAATAAGGCC TGCAAATCGT TTCCCTTCGC ATAGGAAGTC TTTTTTTGCA	360
30	GAAAATCTAC GGGCATCTCC CCCCCTAGTT CCCGTTGCCG TCGACAAGTA TGCGGTACCG	420
	GTTGCCAATC CAATGGATCC TGAAAATCCC AATGCCTGGG ATGTGACGCT AAAAATCACT	480
	ACTAAAGCGG TAACAGTACC TGTCGATGTG GTGATGGTTA TCGACCAGTC TTCGTCAATG	540
	GGAGGGCAAA ACATTGCCAG ATTAAAGTCT GCCATTGCAT CGGGACAGCG TTTTGTGAAA	600
	AAAAATGTTGC CTAAGGGGAC GGCTACAGAA GGGGTGCGTA TCGCTCTTGT GAGTTATGAC	660
35	CATGAGCCTC ATCGCTTATC TGATTTTACC AAAGACACTG CTTTCTCTG TCAAAAAATC	720
	CGGGCTTTGA CTCCTATTTG GGGAACACAT ACCCAGGGGG GGCTTAAAT GGCGAGAAAC	780

	ATTATGGCCA	CTTCTACTGC	TGTGGATAAG	CATATCATAT	TGATGTCTGA	CGGGTTAGCG	840
	ACGGAGCAGT	ATCCTGTAA	AAATGTAAC	ACTGCAGACT	TCATTGGCAA	AACTGGAAAT	900
	GCGAATGATC	CCATTGATTT	GGTTATACAA	GGAGCAATTA	ATTTCCCTAC	AAATTATGTT	960
	TCCAACAATC	CATCTACACC	TCTTACCCCA	AATTATCCAA	CTCATTCTTC	TAAAGTTGGA	1020
5	CGGAGAAATC	TGCCGGAATC	CAAATTTCGAT	TATAGTAATC	TGAGTGCAAG	GATTACTTTT	1080
	GATGGTGTG	CTGGCGCATT	GGTCTATGAA	CCGAGGTTTC	CTCATCCCTA	TTATTATTAT	1140
	TTCCCTTGTA	ACGCTGCTAT	CAATGAGGCT	CAGTTTGCGA	AAAACCTCTG	TTATACAATC	1200
	CATACTATTG	GCTATGACCT	GGGAGATTTT	GCCTTGGCCA	ACAATTTCGT	GAAACTAACC	1260
	GCTACAGACG	AGAATCACTT	CTTTACGGCG	ACACCGGCCA	ATTTAGCTGC	AGCGTTTGAT	1320
10	AATATTGCCC	AAACTATTAA	TATAGGTATA	CAGAGGGGGG	AGGTGACGGA	CTTTGTAGCT	1380
	CCTGGTTTCA	TCGTTAAAAA	TCTGACGCAA	TCGGGAGATG	TTACTCATTT	GCTAAATGTT	1440
	TCAAATGGAA	CGGTGCACTA	TGATGTCTCT	ACTAAAAAAC	TGACATGGAC	TACTGGTACT	1500
	ATCCTGAGCT	CATCAGAAGC	TACCATAACT	TATCGTATTT	ATGCCGATTT	GGATTATATA	1560
	CAGAACAAATG	ATATTCCGGT	AAATACTACT	TCTGCTATCG	GCCCGGATCT	TGGTGGATTC	1620
15	GATACCAATA	CCGAGGCAAA	ATTGACCTAT	ACCAATTCCA	ATGGCGAACC	GAATCAGCAG	1680
	TTAATTTTCC	CACGTCCGAC	GGTTAAGTTA	GGTTATGGTG	TTATTAAGCG	GCACTATGTA	1740
	TTGGTAAATA	AAGACGGTCA	ACCCATACAG	GCAAATGGAA	CAGTTGTCAG	TTCCCTAAGC	1800
	GAGGCTCATG	TTCTACAGTC	ACAAGATTTT	TTTTTGCCCT	CAGGTGGAGG	TCATATTGTT	1860
	CCCAAATGGA	TAAAGTTGGA	CAAAACGACC	GAAGCATTAC	AGTACTATTC	CGTACCGCCG	1920
20	ACTAACACGG	TCATCACTAC	TGCCGATGGT	AAACGTTATC	GTTTTGTCTG	AGTCCCAGGC	1980
	TCCACGCCGA	ATCCGGGCCA	AATCGGTATC	AGTTGGAAAA	AACCGGCAGG	AAACGCTTAC	2040
	TTGCTTACA	AGCTCCTCAA	TTATTGGATG	GGAGGAACAA	CAGACCAACA	GAGTGAATGG	2100
	GATGTGACGT	CCAATTGGAC	AGGAGCCCAA	GTACCGCTCA	CAGGAGAAGA	TGTAGAGTTT	2160
	GCAACGACAG	AAAATTTTCG	TTCTCCGGCG	GTAGCCGATT	TGCATGTCCG	GACAACCAAC	2220
25	CCCAAATTA	TCGGTAACCT	TATCAATAAT	TCCGACAAGG	ATTTAGTTGT	TACCACAAGC	2280
	AGTCAATTGA	CGATCAACGG	CGTGGTTGAG	GATAACAATC	CGAATGTCGG	TACGATCGTC	2340
	GTGAAGTCGT	CGAAAGACAA	TCCTACGGGG	ACATTGCTTT	TTGCCAATCC	GGGCTATAAT	2400
	CAAAATGTAG	GGGGGACCGT	CGAGTTTTTAC	AATCAGGGAT	ATGATTGTGC	CGATTGTGGT	2460
	ATGTATCGCA	GGAGCTGGCA	GTATTTTCGGT	ATCCCTGTCA	ATGAATCAGG	TTTTCCAATT	2520
30	AATGATGTGG	GCGGAAACGA	GACCGTCAAC	CAATGGGTTG	AGCCTTTCAA	TGGCGATAAG	2580
	TGGCGGCCAG	CACCTTATGC	ACCTGATACA	GAGCTTCAAA	AATTCAAGGG	CTACCAGATC	2640
	ACGAATGACG	TGCAGGCACA	GCCTACGGGA	GTTTACAGCT	TCAAGGGTAT	GATTTGTGTG	2700
	TGCGATGCCT	TCCTGAATCT	GACACGCACG	TCCGGTGTCA	ACTACTCGGG	CGCCAACTTG	2760
	ATCGGCAACT	CATACACTGG	AGCCATCGAC	ATCAAGCAGG	GTATTGTCTT	CCCGCCGGAA	2820
35	GTCGAGCAGA	CGGTGTATCT	GTTCAACACG	GGAACACGCG	ACCAGTGGCG	TAAGCTTAAT	2880
	GGAAGCACGG	TTTCAGGCTA	TCGAGCCGGT	CAGTACCTCT	CTGTACCTAA	GAATACAGCG	2940

5 GGTCAAGGACA ATCTTCCGGA TCGTATTCCA TCGATGCATT CCTTCTTGGT GAAGATGCAG 3000
 AACGGAGCGT CTTGTACGTT GCANATCTTG TACGATAAGC TGCTCAAGAA CACGACTGTA 3060
 AACAAACGGTA ATGGTACGCA GATCACATGG CGATCCGGCA ACTCCGGATC GGCGAATATG 3120
 CCGTCACTTG TGATGGATGT TCTTGGAAC GAGTCGGCCG ACCGTTTGTG GATCTTTACC 3180
 5 GATGGGGGTC TTTCTTTCGG ATTCGACAAC GGCTGGGATG GTCGCAAGCT GACTGAAAAA 3240
 GGTTTGTCAC AACTTTATGC GATGTCTGAC ATCGGTAATG ATAAATTCCA GGTTCAGGG 3300
 GTTCCGGAGT TGAATAACCT GCTGATCGGC TTCGATGCGG ATAAGGATGG TCAATACACG 3360
 TTGGAGTTTG CTCTTTCGGA TCATTTTGCG AAAGGGGCTG TTTACCTGCA CGATCTTCAG 3420
 TCAGGAGCCA AACACCGTAT TACGAATTCT ACGTCGTATT CATTTCGATGC CAAGCGGGGA 3480
 10 GATTCCGGGG CTCGTTTCCG CTTGTCATAT GGATGTGATG AGAACGTAGA TGATTTCGCAT 3540
 GTCGTGAGTA CAAATGGCCG TGAAATTATA ATTCTGAATC AAGATGCTCT TGAATGCACT 3600
 GTAACCTTAT TCACAATAGA AGGTAAGCTT CTTGCCGCT TGAAAGTATT AGCTGGTCAT 3660
 AGAGAAGTCA TGAAAGTGCA GACCGGAGGG GCCTATATTG TGCATCTTCA AAATGCTTTC 3720
 ACTAATGATG TGCATAAGGT GCTTGTTGAG TAT 3753
 15

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- 25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

35

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

	ACTATGGAAG TGAAGAAAAA CACAGTGGTG CTACGCCTTC TGATTTGGTT CGTGGCCATT	60
5	CTTCTCTTCC ACTCCTCACG GCTGTGGGGA CAGGAAGGGG AGGGGAGTGC CCGATACAGA	120
	TTCAAAGGAT TCGTGGATAC CTACCATGCC GTACGCAGCT CTTCTCCTTT TGATTTTCATG	180
	AGCTCGCGTA CGAGAGTGAG AGGTGAGCTG GAGAGGTCGT TCGGTAATTC GAAAGTAGCC	240
	GTATCGGTCA ATGCCACCTA CAATGCTCTA CTGAAAGACG AGACCGGCTT ACGTTTACGT	300
	GAAGCCTTCT TCGAGCATCA GGAAGAGCAT TGGGGGTTGC GCCTCGGACG ACAGATTGTC	360
10	ATTTGGGGGG CTGCCGACGG TGTGCGCATC ACGGATCTGA TCTCCCCGAT GGATATGACC	420
	GAGTTTCTGG CACAGGATTA CGATGATATT CGTATGCCGG TCAATGCATT GCGTTTCTCT	480
	GTCTTCAACG AATCGATGAA AGTGGAAGTC GTGGTACTGC CTGTATTCTGA GGGGTACCGT	540
	CTGCCTGTGG ATCCTCGCAA TCC'TTGAAT ATCTTCTCCC TTTCGCCCCAT TGCTCAGGGG	600
	ATGAATATCG TCTGGAAGA AGAAGCCGGC AAACCGGCCT TCAAGGTTGC CAATATCGAG	660
15	TACGGTGCGC GATGGAGCAC TACGCTCTCC GGTATCGACT TCGCTTTGGC TGCATTGCAT	720
	ACATGGAACA AGATGCCCCG CATCGAAGTA CAGGGCATTG TGCCGACGGA AATCATCGTT	780
	AGCCCTCGCT ATTATCGTAT GGGATTTGTC GGCGGCGACC TCTCCGTACC CGTCGGACAG	840
	TTTGTTTTCA GGGGAGAGGC TGC GTTCAAT ATCGACAAAC ACTTCACCTA TAAGAGTCAT	900
	GCCGAGCAAG AGGGTTTCCA AACAATCAAT TGGTTGGCCG GAGCCGATTE GSTATGCTCCC	960
20	GGTGAATGGA TGATCTCAGG ACAATTCTCA ATGGAAAGCA TATTCAGGTA TAGGGATTTC	1020
	ATCTCCCAA GACAACATTC TACCCTGATT ACTCTCAATG TTTCCAAGAA ATTCTTCGGC	1080
	AGTACACTCC AACTTTCGGA CTTACCTAC TACGACCTTA CGGGCAAAGG ATGGTTTCAGT	1140
	CGCTTTGCAG CTGACTATGC CTTGAACGAT CAGATACATC TGATGGCCGG ATATGACTGG	1200
	TTCAGTAGTA AGGGCAGCGG TATATTCGAT CGCTACAAAG ACAATTCCGA ACTCTGGTTC	1260
25	AAAGCCCGCT ACAGCTTC	1278

(2) INFORMATION FOR SEQ ID NO:40

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

35

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

10

(A) NAME/KEY: misc_feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

15	AGGGGGTCGA GTTCGGGCAT TTCAGCCCGT GGACGCGACA TCGTTCTTT ATTTTGGAGC	60
	GCGTTGCGCA GCTCCTCTCT CCATGGTTCA GAGCGACGCA GTCGGATAAG TTCTTCTGTA	120
	GTCATGTCAA TAAGGCAGAA AATAAGGTTA TTCCATCTCT CGGTATGCGC CCAAACGCAT	180
	GATCATCTCA TCGAAATCCA CTTGGTGTGC ATCGAATTCT GGGCCATCGA CACAGACGAA	240
	TTTCGTCTGT CCTCCACGC TTATACGACA AGCCCCACAC ATACCGGTGC CATCCACCAT	300
20	AATTGTATTG AGAGAAGCTA TGGTCGGTAT CTCGTAACGT TTGGTCAGGA GAGAAACGAA	360
	CTTCATCATC ACAGCCGGCC CGATCGTAAC GCAGAGGTCT ACCGTTTCCC GTTTGATAAC	420
	GCTTTCCACT CCATCCGTTA CGAGGCCTTT CGTCCCATAA GACCCATCGT CTGTCATGAT	480
	GATCACTTCA TCGCTATTGG CTCGCATTTG TTCTTCAAGG ATAACCAGAT CTTTAGTTCT	540
	GGCAGCCAAT ACGACAATTA CACGGTTGCC TGCTTTGTGG AAAGCCTCCA CGATCGGGAG	600
25	CAAAGGAGCC ACACCCACAC CGCCTCCGGC ACAAACCACT GTGCCGACCT TTTCGATATG	660
	CGTACTCTGT CCCAGCGGAC CTACCACATC CGTGATATAG TCGCCGACTT CGAGTTCGGC	720
	CAATTTCTTG GAAGATTGTC CCACGGCCTG AACCAC	756

30 (2) INFORMATION FOR SEQ ID NO:41

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

10

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...798

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

	ATAATTTATA GATCAACAAT GAAACTATTA CTTTATCTCC TATTGGTCTT GTCGACTCTA	60
	TCCCCGATGT ATTGCGAAAT GCTCTTCTCA GAGAATCTCA CAATGAATAT AGACAGCACC	120
	AAAACCATAC AAGGAACGAT ATTGCCCCGTA CTGGATTTCA AAACCGAAAA GGAAAATGTG	180
20	TTCACCTTCA AAAATACTGC CAATCTCAAT CTGCTGATAA AGCACGGTCA AGTAATCAAC	240
	TTAATTAATA AGCTTGAGTT TTCTACCTAT GGCAATAAAG TAACCGTAAG TGGAGGATAT	300
	GTACACACCG AATACCGCTA TTTGTTGTCAT CATGTTTTTG AGGTTTATCC TTATGTCGAG	360
	TCGCAATGGG CAGAAAGTAG AGGAATGAAA TATAAGGTTT CTACGGGATT ACAGTCGCGT	420
	TATCGGCTGG TAAATAGTGA TAACTGTCTC ATGTTTGCAA CATTGGGGGT ATTTTTCGAA	480
25	TTCGAAAAGT GGGAACAGCC AGCCACTAGC CTCTTTGCAG GAACGTATGC ATACAGCCGA	540
	AGTATCAAAA GCCACCTGTC TATCAGTTTC AGACATCGGT TGGGTGAACA TTGGGAATTT	600
	ACAACTACGG CTATTCACCA GGGAAAGCCT GACAGTTATT TTAAGAAGGC ACGTTTTGGA	660
	GGAGCTATCG ACCTCAAATA CCATATCACA CCTACGATAG GAATACGCGG GGCCTATCGG	720
	ATCATCTACG ATACTGCCCC TATTGTACCT GTGCGGAAAG ATTACAACAC CGTTGATGTT	780
30	GGTATCGATA TTTCGTTT	798

(2) INFORMATION FOR SEQ ID NO:42

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 987 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

15

(A) NAME/KEY: misc_feature

(B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

20	GAGACGAACT CTTGGGTATC CAGCGATTGC AATTCGACGA CGATGAAAAC GAATAGACGA	60
	TACGCATTTG TTTTGCCGCT TCTGCTACTC ACCGGATTGT TGGCATGGGG GCAGGATTCT	120
	TCCCACGGTA GCAATACAGC GTTTGCAACT GATTCTTCGA GTAGAGAGTT GCCCACGGAG	180
	CAGTCCGCCT ACCGCATTCA TTCTGCCTAT ATGGTCGGTG GTGGCGGAAG CATAACGCGC	240
	GACACCTATT TGTCACCCCT TCGTTATGGA GGATGGACAC TGAATTTGTL GGGAGAGAAG	300
25	ACGTTCCCTC TCAAAGCCTC CGATTCCCGT TGGATGATCC GTACCGGGCA TGAGCTGGAT	360
	TTTGCCCTGA TGGACAATCC GGCCAATAAT GCTCATTTCT ATTCCCTGCT GTATAACGGT	420
	TCCGCTGCGG CTCTTTACCG CCTTGGCGCT AAGCATCTGC GAGCCGCGTG GATGGACAAT	480
	CTGCGCTTGG CATTCGGCCC GGGCTTGGA ATCGGGCTTG GAGGAATTTA TAGTACACGC	540
	AACGGCAATA ATCCTGCGAC ATTGAAGCTC TACACCAATG CCATCGCCCA AGCCTCGATA	600
30	GGATACTACG TCCCCTCCGA AACTTTTCCC CTGTATTTTC GGTGCTCTC CCAGATCAAT	660
	CTCTTCGGTA TAGCCTATGG AAATGGTTTT GGTGAGAGCT ATTACGAGAA TTTTTTGCTC	720
	AATAACGGCA TTGCAGGCTC CCTGCATTTT ACTTATCCGG GCAAGTTTAC TCGGTTACAG	780
	ACACTCATAA CGGCGGATAT TCCCATTCGG AACTTCTGTA CGCTTCGTGT CGGTTATCGC	840
	TATTCCCATT TGGGCTCTTC GCTTAACGCA TTGGATACTC GAATCCACAG TCATACGGCT	900
35	TTTATCGGTT TCGTCACGGA GTTTTACCGA TTCCGTGGGC GCAAAGCCAT GAATACGGT	960
	CGGAGAACCA GTCTTTACTA TCATGAT	987

(2) INFORMATION FOR SEQ ID NO:43

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

20

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

25

CCCCGTTTTC ATCCCGGAGG GACACACGCT CAGCTTTGCA GAAATGGGAG AAGAAACCAA	60
AAATCAAATC AGTCATCGTG CTTTGGCGGT GGCACAGCTC CGCGATTTTT TATTATGTGC	120
AAAATAAGAT TCAGCCTCTT GCAGGCTCTT GTCGTCTGCT TATTGTTTAC CTCTTTTTCT	180
CTCCAAGCTC AAGAGGAAGG TATTTGGAAT ACCCTCTTGG CTATCCACAA GACGGAAAAA	240
30 GCCGTAGAAA CGCCAAGAA AGTCTTTGCC GTAGCCAACG GAGTACTTTA CTCGGTGGGC	300
AAAGAAGCTC CCCATGAGGC AAAGATCTTC GACCGTATCA GCGGACTCAG CGATACATCG	360
GTAAGCAGCA TAGCCTACTC CGAGCAACTA AAATCCTTGG TCATATACTA TGCATCAGGC	420
AATATCGACA TCTTGGACGA AGCAGGCCGT GTGACCAACG TACCTGCATT GAAAGACAAT	480
ATCGATCTGA TAGACAAAAC GCTCAATCGC CTTTGTATCG TAGGCAACAG GGCTTATTTG	540
35 GCAGGAGGAT TCGGCCTCTC CGTTCTGGAT GTCGCCGAAG CTCGCATACC GGCTACCTAC	600
GCCAAGGGAA CTAAGGTGAC CGATGTGGCT AAGTTGGACA ATGATCGCTT GCTGATGCTG	660

	AAAGAAGGGC	AGCTCTTCAT	CGGAAAAGAG	ACCGATAACC	TGCAAGATCC	GGCCGCATGG	720
	ACAGCCTTGT	CTTTGAATTT	GCCGATGGGC	TCGGTCACCG	GTCTGGGCAT	TGTCGGGGAA	780
	GACATCTGTT	TCCTGCTCGC	CGATGGCCGT	GTATATGTCT	CTGCAAACCA	ATCGTTTGAG	840
	CCGGAGCTAT	TGCTCTCTTC	CTCCGCCGAT	TCACGACTGT	ATGTGACGGA	TCGTGGTCTG	900
5	TTCATCTGTG	CCGAGAATCG	AATTTATTTT	ATAGAAAAAG	GTCGCAAAAC	GACACAATTT	960
	CCTATAGCCG	ACGTCCTTGG	TGTCGGTGCC	ATGAACGAAA	GCAATACGGC	ATACATAGCA	1020
	TTGGGAGAAG	AAGGTTTGGC	TTCACCTCTT	CTCGCAGAGG	GAAGTACGGC	CGAAGCCATG	1080
	CCTGTAGCAT	TCGACGGACC	GGGGGACAAT	GATTTCTACG	AGATGCGGTT	TAGTCACGGA	1140
	CGTCTGTATG	CAGCCAGCGG	ACTCTGGGGA	ACAAACCTGA	TGGGACATGC	CGGTATGGTG	1200
10	AAGCTATACG	ACGGCAACCG	ATGGACTAAC	TTTCACAAGA	AGACCGTACA	GGAACAGTTG	1260
	GGCGCGGAT	TCAGTTTCAA	TGATGCTATC	GATATAGCTG	TTTCCAACGG	AGACCCCGAT	1320
	CACFTTTTTT	TCGGTACATG	GGGAAACGGT	CTGTTCGAAT	TCAAGGATGG	CAAAGCGATA	1380
	GCTCGCTATT	CGGGAAACGA	AACTGCTATC	GCAGAATGTA	ATCCCGGAGA	TGCCCCGTGT	1440
	AAAGCGATTG	CCTTTGACAA	TAAGGGCAAC	CTCTGGGGGA	CGCTCGGTGC	CGTAGGCAAG	1500
15	AACATCTTCA	TGTACGATCC	GCAGAGTAGC	ACATGGCATT	CTTTCAGCTA	TCCGGATGTA	1560
	GCCAATCTGG	CCTCCTTCGG	CAATATGATT	ATCCTACCCA	ACGGAGACAA	ATGGGTAAAT	1620
	ATCCTTCACC	GTAGTGGCGG	ATCCACGCGC	AAAGGTGTCT	TGATCTTCAA	CGATCGGGGT	1680
	ACACCGGAAA	CGACTTCGGA	CGACAGCCAT	CTTTACGTCG	AGCAGTTTGT	CAATCGCCTC	1740
	GGGGCAGCCA	TAGGACATAA	GACTATCTAT	GCAATGGCCG	TCGATCATAA	CGGCTCTGTC	1800
20	TGGATGGGAT	CGGATATAGG	CATTTTCGGC	GTCTACAATG	CAGCCGGAGT	ATTGTCCTCG	1860
	ACTTCTACCC	CTATCGCTGT	TCGGCCGGTC	GGAGGAGAAG	AACCCAATTT	GTACTATGTG	1920
	CTGGACAAGG	TGACGGTGAC	AGACATCGTC	GTGGACAAAC	TCAATCACAA	ATGGGTTGCC	1980
	ACCCAAGGGA	CAGGACTCTA	TCTCCTTTTC	GAAGATTGCA	GTAAGATCCT	CGCGCAATTT	2040
	ACCGTAGAAA	ACAGCCCTTT	GCTTTCTAAC	AACATACTAT	CCCTGGCCTT	AAATGACGAT	2100
25	AACGGACTGC	TGTACATCGG	TACGGCGGAC	GGACTGATGA	CGTTCCAAAC	GGGTACGGGG	2160
	AGTGGATCAG	CTTCCGAAC	GGACGGCGTC	TATGTATACC	CCAATCCGCT	AAGGCCGGAA	2220
	TATCCCGATG	GCGTCACCAT	TGCCGGACTG	CAAGCCGGCT	GTAGTGTCAA	AATCACCGAT	2280
	ACCACCGGCA	GACTGCTATA	CCAGACTGAG	AGCGTAACCA	CCGAAGTCAA	ATGGAATGCT	2340
	CGAGGTGCCG	ATGGCAATAG	GGTAGCTTCG	GGCGTATATG	CCGTTGCAGT	GTACGATCCG	2400
30	GTATCGAAAA	AGTCCAAACT	AATTCGCTTC	GCASTGATTC	GC		2442

(2) INFORMATION FOR SEQ ID NO:44

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1353 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

15

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

20	AAAACATCAT ATCGGAATAA TATGCGTTTC CAACATTATC TCATCTGTAC GGCTGCCGTA	60
	GCGGCTTTGG CTGCGAATCC CCTTACGGGC CAATCGAATA TGACCCCTCGA AGAGTGCATA	120
	GACTATGCAC GCCGGCACAG TTCGGCCGTG GCGCTGTCCG CTGCGGAACT GGAGCAGTCC	180
	AAGGCCGATT ACCTTCAGGC CGTCGGCAAT TTTCTGCCCC GTGTATCGGC CGGAACCGGT	240
	GCTTCGTGGA ATTTTCGGACG CGGATTGGAT GCCGAGACGA ATACCTACAG CGACATCAAC	300
25	AGCTTCAACA ATTCGTACAG CATAATGCC ACGATGACCC TTTTCGACGG TTTGCAGAGT	360
	GTCTATCGAC TGCGGATGGC GCATGCACGC CGGGAGGCTT CGCGCCTCTC CGTTCGCGAG	420
	CAGCAGGAGC TGGCAGCTCT CGGCACCACG GAGGCCTACT ACGACCTCGT CTATGCGCGC	480
	CAAATGCAAG AGCTGGCCAT GCAGAAGTAC GAGGAGAGCA GCCGCCTCCA CCGGCAGACG	540
	GCTCGAATGG AAGAGCTGGG GATGAAGAGT CGTCCCGATG TCCTCGAGAT GCAGTCGCGA	600
30	ATGGCCGGTG ACCGTTTGGC CCTGACTCAA GCGGACAATC AGTGCATCAT CGCTCTGATC	660
	CGGCTCAAAG AAAAAATGAA CTTCCCCATC GATGACGAAC TCGTCGTAGA CGATATGCCG	720
	GCTGACAGTC TCTCCGCCGA CATGGCCGAA TCGGACAGCT CGGCCGGCGT CTTCGCCCCG	780
	GCTGCCCCATC ATCATCCCGT CCTCCTCCGT GCCAACTCG ACGAGCAGGC TGCCACCGAC	840
	CGTTTGCGAG CCGCGCGAGG TGCATTCCCTG CCGAGTGTGT CGGTATCCGG AGGATGGAAC	900
35	ACGGGATTCT CACGCTTTTT GAATGGATCG GACTATACGC CCTTCAGCGA GCAGTTTCGG	960
	AACCGTCGGG GGAATACGT CAGTCTGAAT CTGAGTATCC CCATCTTTTC GGGATTACAGC	1020

CTTGTGAGCC ATCTGCGTCA GGCGCGTGCC GAACGCAGGG CGGCAATCGT CCGACGGGGC 1080
 GAAGCGGAGC GCAGGCTCTA CAGCGAGATC GCCCAAGCCA TGGCCGACCG GGATGCCGCT 1140
 CTGGCTTCCT ACCGCCAGGC GAAGGAGCAT ACCGACGCCA TGCAAACCGC TTACGAAGCC 1200
 GTCTTGCAGC GTTATGAGGA GGGGCTGAAT ACGGCCATCG ACCTGACCAC TCAGGCCAAT 1260
 5 CGGCTCCTGG ATGCCCCGTGT GCAGCGACTG AGAGCGGCCA TGACCTACCG GCTCAAATGC 1320
 AAACTCATAG CCTATTACGG CTGCCTTTCG GAC 1353

10 (2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 589 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

25 (A) NAME/KEY: misc_feature

(B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

30 Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu Gln
 1 5 10 15
 Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val Val
 20 25 30
 Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser Gln
 35 35 40 45
 Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro Ala

	50		55		60	
	Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala Thr					
	65		70		75	80
	Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala Ala					
5		85		90		95
	Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu Val					
		100		105		110
	Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly Phe					
		115		120		125
10	Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys Thr					
		130		135		140
	Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile His					
	145		150		155	160
	Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys Arg					
15		165		170		175
	Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro Asp					
		180		185		190
	Asn Thr Ala Lys Pro Tyr Tyr Tyr Arg Val Pro Leu Glu Ser Gln Asp					
		195		200		205
20	Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile Glu					
		210		215		220
	Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly Thr					
	225		230		235	240
	Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu Pro					
25		245		250		255
	Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn Asn					
		260		265		270
	Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile Ser					
		275		280		285
30	Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly Thr					
		290		295		300
	Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr Ile					
	305		310		315	320
	Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val Asn					
35		325		330		335
	Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala Gly					

	340	345	350
	Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile Val		
	355	360	365
	Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu Ala		
5	370	375	380
	Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val Pro		
	385	390	395 400
	Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr Pro		
	405	410	415
10	Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr Pro		
	420	425	430
	Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr Ser		
	435	440	445
	Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala Thr		
15	450	455	460
	Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu Leu		
	465	470	475 480
	Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn Cys		
	485	490	495
20	Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys Phe		
	500	505	510
	Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp Lys		
	515	520	525
	Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly Asn		
25	530	535	540
	Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln Gly		
	545	550	555 560
	Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val Arg		
	565	570	575
30	Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys		
	580	585	

(2) INFORMATION FOR SEQ ID NO:46

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...907

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

	Thr	Ile	Cys	Val	Ala	Phe	Leu	Ser	Ala	Pro	Val	Ala	Ala	Leu	Arg	Glu
	1				5					10					15	
	Ser	Pro	Pro	Met	Gly	Ala	Glu	Arg	Lys	Thr	Pro	Ser	Leu	Leu	Pro	Leu
20				20					25					30		
	Leu	Phe	Glu	His	Ser	Asp	Lys	Gly	Lys	Gly	Phe	Asp	Tyr	Arg	Leu	Phe
				35					40					45		
	Thr	Ser	Asn	Lys	Leu	Lys	Val	Phe	Ala	Thr	Gly	Asn	Ser	Arg	Tyr	Ile
				50					55					60		
25	His	Asn	Lys	Pro	Thr	Ile	Ile	Gln	Ala	Met	Lys	Arg	Ile	Val	Leu	Ser
	65					70					75				80	
	Ser	Phe	Leu	Phe	Val	Leu	Ser	Ile	Leu	Ser	Leu	Met	Ala	Gln	Asn	Asn
					85						90				95	
	Thr	Leu	Asp	Val	His	Ile	Ser	Gly	Thr	Ile	Lys	Asp	Ala	Ser	Ser	Gly
30					100					105					110	
	Glu	Pro	Val	Pro	Tyr	Ala	Thr	Val	Ser	Ile	Arg	Leu	Thr	Gly	Ala	Asp
					115					120				125		
	Thr	Thr	Gln	Val	Phe	Arg	Gln	Val	Thr	Asp	Gly	Asn	Gly	Tyr	Phe	Val
				130					135					140		
35	Ile	Gly	Leu	Pro	Ala	Ala	Pro	Ser	Tyr	His	Leu	Thr	Ala	Ser	Phe	Val
	145						150					155				160

Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His
 165 170 175
 Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu
 180 185 190
 5 Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile
 195 200 205
 Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Ala Lys Thr Asn
 210 215 220
 Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly
 10 225 230 235 240
 Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu
 245 250 255
 Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe
 260 265 270
 15 Arg Ser Ile Pro Ala His Thr Ile Lys Arg Val Glu Val Ile Thr Asp
 275 280 285
 Pro Gly Val Lys Tyr Asp Ala Glu Gly Thr Ser Ala Ile Leu Asp Ile
 290 295 300
 Val Thr Glu Glu Gly Lys Lys Leu Glu Gly Tyr Ser Gly Ser Ile Thr
 20 305 310 315 320
 Ala Ser Val Ser Asn Asn Pro Thr Ala Asn Gly Ser Ile Phe Leu Thr
 325 330 335
 Ala Lys Ser Gly Lys Val Gly Leu Thr Thr Asn Tyr Asn Tyr Tyr Gly
 340 345 350
 25 Gly Lys Asn Lys Gly Ser Arg Tyr Phe Thr Glu Arg Thr Thr Ser Met
 355 360 365
 Leu Gln Thr Ile Glu Glu Gly Lys Gly Gln Glu Thr Phe Gly Gly His
 370 375 380
 Phe Gly Asn Ala Leu Leu Ser Phe Glu Ile Asp Ser Leu Asn Leu Phe
 30 385 390 395 400
 Thr Val Gly Gly Asn Val Arg Leu Trp Glu Met Thr Thr Asp Arg Asn
 405 410 415
 Ser Val Glu Lys Ser Phe Ala Gly Ser Asn Leu Met Ser Tyr Ile Asp
 420 425 430
 35 Arg Lys Leu Lys Thr Gln Met Asp Ala Gly Ser Tyr Glu Leu Asn Ala
 435 440 445

	Asp	Tyr	Gln	His	Ser	Thr	Arg	Leu	Pro	Gly	Glu	Leu	Leu	Thr	Val	Ser	
	450							455				460					
	Tyr	Arg	Phe	Thr	His	Asn	Pro	Asn	Asn	Ser	Glu	Thr	Phe	Ile	Asp	Gln	
	465					470					475					480	
5	Trp	Lys	Arg	Asp	Pro	Leu	Asn	Thr	Ala	Asn	Thr	Ile	Gln	Tyr	Ala	Gly	
						485				490					495		
	Gln	His	Ser	Lys	Ser	Asp	Ala	Gly	Met	Asp	Glu	His	Thr	Ala	Gln	Val	
				500					505					510			
	Asp	Tyr	Thr	Arg	Pro	Leu	Gly	Gln	Ala	His	Ser	Leu	Glu	Ala	Gly	Leu	
10			515					520					525				
	Lys	Tyr	Ile	Tyr	Arg	His	Ala	Thr	Ser	Asp	Pro	Leu	Tyr	Glu	Ile	Arg	
	530						535						540				
	Pro	Ser	Glu	Asp	Ala	Pro	Trp	Gln	Pro	Gly	Ser	Leu	Tyr	Ala	Gln	Asn	
	545					550					555					560	
15	Pro	Ser	Asn	Gly	Lys	Phe	Arg	His	Asp	Gln	Tyr	Ile	Gly	Ala	Ala	Tyr	
						565				570					575		
	Ala	Gly	Tyr	Asn	Tyr	Arg	Lys	Asp	Gln	Tyr	Ser	Leu	Gln	Thr	Gly	Leu	
				580					585					590			
	Arg	Val	Glu	Ser	Ser	Arg	Leu	Lys	Ala	Leu	Phe	Pro	Glu	Asn	Ala	Ala	
20			595					600					605				
	Ala	Asp	Phe	Ser	His	Asn	Ser	Phe	Asp	Trp	Val	Pro	Gln	Leu	Thr	Leu	
	610						615					620					
	Gly	Tyr	Thr	Pro	Ser	Pro	Met	Lys	Gln	Leu	Lys	Leu	Ala	Tyr	Asn	Phe	
	625					630					635					640	
25	Arg	Ile	Gln	Arg	Pro	Ala	Ile	Gly	Gln	Leu	Asn	Pro	Tyr	Arg	Leu	Gln	
						645					650				655		
	Thr	Asn	Asp	Unk	Gln	Val	Gln	Tyr	Gly	Asn	Pro	Asp	Leu	Lys	Ser	Glu	
				660					665					670			
	Lys	Arg	His	His	Val	Gly	Leu	Ser	Tyr	Asn	Gln	Tyr	Gly	Ala	Lys	Val	
30			675						680				685				
	Met	Leu	Thr	Ala	Ser	Leu	Asp	Tyr	Asp	Phe	Cys	Asn	Asn	Ala	Ile	Gln	
	690						695					700					
	Asn	Tyr	Thr	Phe	Ser	Asp	Pro	Ala	Asn	Pro	Asn	Leu	Phe	His	Gln	Thr	
	705					710					715				720		
35	Tyr	Gly	Asn	Ile	Gly	Arg	Glu	His	Ser	Phe	Ser	Leu	Asn	Thr	Tyr	Ala	
						725					730				735		

Met Tyr Thr Pro Ala Val Trp Val Arg Ile Met Leu Asn Gly Asn Ile
 740 745 750
 Asp Arg Thr Phe Gln Lys Ser Glu Ala Leu Gly Ile Asp Val Asn Ser
 755 760 765
 5 Trp Ser Gly Met Val Tyr Ser Gly Leu Met Phe Thr Leu Pro Lys Asp
 770 775 780
 Trp Thr Val Asn Leu Phe Gly Gly Tyr Tyr His Gly Gly Arg Ser Tyr
 785 790 795 800
 Gln Thr Lys Tyr Asp Gly Asn Val Phe Asn Asn Ile Gly Ile Ala Lys
 10 805 810 815
 Gln Leu Phe Asp Lys Lys Leu Arg Val Ser Leu Ser Ala Asn Asn Ile
 820 825 830
 His Ala Lys Tyr Ser Thr Trp Lys Ser Arg Thr Ile Gly Asn Gly Phe
 835 840 845
 15 Thr Ile Tyr Ser Glu Asn Ala Gly Ile Gln Arg Ser Val Ser Leu Ser
 850 855 860
 Leu Thr Tyr Ser Phe Gly Lys Met Asn Thr Gln Val Arg Lys Val Glu
 865 870 875 880
 Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln
 20 885 890 895
 Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn
 900 905

(2) INFORMATION FOR SEQ ID NO:47

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...606

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

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Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser
1           5           10           15
10 Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val
    20           25           30
Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro
    35           40           45
Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu
15    50           55           60
Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro
65           70           75           80
Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe
    85           90           95
20 Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu
    100          105          110
Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile
    115          120          125
Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp
25    130          135          140
Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys
145          150          155          160
Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg
    165          170          175
30 Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu
    180          185          190
Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg
    195          200          205
Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val
35    210          215          220
Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly

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	225	230	235	240
	Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg			
	245	250	255	
	Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His			
5	260	265	270	
	Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile			
	275	280	285	
	Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn			
	290	295	300	
10	Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu			
	305	310	315	320
	Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp			
	325	330	335	
	Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe			
15	340	345	350	
	Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu			
	355	360	365	
	Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val			
	370	375	380	
20	Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu			
	385	390	395	400
	Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln			
	405	410	415	
	Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr			
25	420	425	430	
	Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu			
	435	440	445	
	Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu			
	450	455	460	
30	Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu			
	465	470	475	480
	Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly			
	485	490	495	
	Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu			
35	500	505	510	
	Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val			

	515		520		525											
	Arg	Leu	Arg	Tyr	Thr	Gln	Leu	Asn	Gly	Arg	Tyr	Arg	Tyr	Ser	Phe	Gly
	530		535		540											
	Ser	Ala	Gly	Ser	Glu	Ala	Leu	Gly	Ile	Gly	Asn	Val	His	Leu	Leu	Ser
5	545		550		555		560									
	Ala	Asp	Val	Ser	Tyr	Lys	Leu	Lys	Lys	Asn	Leu	Ser	Leu	Tyr	Leu	Lys
			565		570		575									
	Ile	Asp	Asn	Met	Leu	Ala	Glu	Thr	Thr	Glu	Leu	Ile	Gly	Tyr	Tyr	Pro
			580		585		590									
10	Met	Gln	Pro	Phe	His	Cys	Phe	Ala	Gly	Phe	Ser	Trp	Thr	Phe		
			595		600		605									

(2) INFORMATION FOR SEQ ID NO:48

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- 25 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

	Asn	Ser	His	Ala	Thr	Val	Ser	Val	Ile	Cys	Ser	Met	Met	Glu	Lys	Cys
	1		5		10		15									
35	Ile	Phe	Ala	His	Tyr	Pro	His	Asn	Leu	Val	Phe	Met	Ile	Arg	Lys	His
			20		25		30									

Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala
 35 40 45
 Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala
 50 55 60
 5 Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn
 65 70 75 80
 Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly
 85 90 95
 Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met
 10 100 105 110
 Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly
 115 120 125
 Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln
 130 135 140
 15 Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln
 145 150 155 160
 Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser
 165 170 175
 Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu
 20 180 185 190
 Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp Lys Gly Tyr Ser
 195 200 205
 Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn
 210 215 220
 25 Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg
 225 230 235 240
 Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu
 245 250 255
 Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met
 30 260 265 270
 Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser
 275 280 285
 Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp
 290 295 300
 35 Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val
 305 310 315 320

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

20 (A) ORGANISM: Porphyromonas gingivalis

(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

	Lys	Phe	Met	Met	Lys	Lys	Ala	Phe	Val	Phe	Val	Leu	Leu	Val	Cys	Leu
	1				5					10					15	
30	Phe	Ser	Ser	Phe	Ser	Ser	Ser	Ala	Gln	Thr	Thr	Thr	Asn	Ser	Ser	Arg
				20					25					30		
	Ser	Tyr	Phe	Thr	Gly	Arg	Ile	Glu	Lys	Val	Ser	Leu	Asn	Leu	Gly	Val
			35					40					45			
	Pro	Pro	Val	Ser	Thr	Glu	Val	Trp	Gly	Met	Thr	His	Asp	Ala	Asn	Gly
35		50					55					60				
	Leu	Pro	Phe	Glu	Ile	Pro	Ile	Ser	Phe	Ser	Arg	Phe	Asn	Ser	Gln	Gly

	65		70		75		80									
	Asp	Ile	Ala	Thr	Thr	Tyr	Tyr	Ile	Ala	Asn	Ser	Glu	Ala	Thr	Leu	Asn
				85				90							95	
	Glu	Trp	Cys	Asp	Tyr	Ala	His	Pro	Gly	Gly	Ile	Val	Arg	Val	Glu	Gly
5				100				105							110	
	Arg	Phe	Trp	Lys	Met	Thr	Tyr	Asn	Ile	Pro	Thr	Tyr	Asn	Ala	Val	Cys
				115				120						125		
	Thr	Arg	Ile	Thr	Phe	Glu	Asn	Gln	Glu	Ile	Glu	Gly	Thr	Ile	Val	Leu
				130				135						140		
10	Ile	Pro	Lys	Pro	Lys	Val	Ser	Leu	Pro	His	Val	Ser	Glu	Ser	Val	Pro
				145				150					155			160
	Cys	Ile	Arg	Thr	Glu	Ala	Gly	Arg	Glu	Phe	Ile	Leu	Cys	Glu	Glu	Asp
					165					170					175	
	Asp	Thr	Phe	Val	Ser	His	Asp	Gly	Asn	Glu	Val	Thr	Ile	Gly	Gly	Lys
15				180					185						190	
	Pro	Phe	Leu	Leu	Asn	Thr	Asn	Val	Lys	Ile	Val	Gly	Asp	Val	Ser	Gln
				195				200						205		
	Lys	Tyr	Ala	Val	Gly	Val	Gly	Glu	Ile	Arg	Phe	Leu	Gln	Ile	Cys	Ala
				210				215						220		
20	Gln	Thr	Val	Ser	Gln	Gln	Lys									
				225			230									

(2) INFORMATION FOR SEQ ID NO:50

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 566 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...566

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

```

Tyr Asp Gly Ala Arg Leu Val Tyr Thr Leu Phe Arg Asn Arg Asn Asp
1           5           10           15
Ile His Pro Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala
10          20          25          30
Leu Phe Phe Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln
          35          40          45
Met Leu Asn Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro
          50          55          60
15 Thr Glu Arg Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg
          65          70          75          80
Gly Ala Asp Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr
          85          90          95
Val Arg Phe Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro
20          100         105         110
Tyr Asn Gly Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg
          115         120         125
Ile Ser Val Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser
          130         135         140
25 Arg Gly Met His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu
          145         150         155         160
Ala Tyr Tyr Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His
          165         170         175
Phe Glu Asp Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg
30          180         185         190
Leu Pro Leu Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg
          195         200         205
Leu Thr Asp Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser
          210         215         220
35 Cys Ala Thr Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser
          225         230         235         240

```

	Ala	Ala	Tyr	Leu	Tyr	His	Arg	Gln	His	Leu	Thr	Gln	Tyr	Asn	Trp	Arg
						245				250					255	
	Pro	Gly	Gln	Gln	Asp	Lys	Phe	Phe	Val	Ser	Tyr	Gly	Phe	Gly	Gln	Val
						260				265					270	
5	Asp	Val	Ser	Asn	Ser	Pro	Ile	Trp	Phe	Gly	Ile	Ser	Arg	Met	Asn	Tyr
						275				280				285		
	Val	Asn	Gly	Trp	Lys	Leu	Ser	Ser	Arg	Leu	Asp	Thr	Arg	Arg	Gly	Asp
						290				295			300			
	Ala	Ile	Gly	Leu	Asp	Tyr	Ser	Gly	Tyr	Phe	Leu	Asp	Thr	Glu	Glu	Arg
10	305					310					315					320
	Ser	Ser	Ile	Asn	Leu	Phe	Ala	Leu	Leu	Tyr	Asn	Arg	Leu	Arg	Leu	Tyr
						325					330				335	
	Gly	Ser	Trp	His	Leu	Ser	Asp	Phe	Asp	Phe	Ser	Phe	Ser	Ala	Asp	Tyr
						340				345				350		
15	Ala	Leu	Arg	Gln	Gly	Ile	Glu	Arg	Ile	Tyr	Glu	Asp	Tyr	Lys	Pro	Asp
						355				360				365		
	Asp	Asn	Tyr	His	Ile	Tyr	Asp	Leu	Arg	Ile	Leu	Ala	Ile	Arg	Arg	Trp
						370				375			380			
	Tyr	Met	Leu	Asn	Glu	Phe	Ser	Ala	Gln	Ala	Gln	Ala	Ser	Tyr	Arg	Ile
20	385					390					395					400
	Arg	Thr	Asp	Arg	Gly	Cys	Ala	Leu	Arg	Val	Ser	Ala	Gly	Ser	Asp	Phe
						405					410				415	
	Tyr	Gly	Tyr	Asp	Glu	Thr	Tyr	Arg	Lys	His	Gly	His	His	Thr	Met	Ser
						420				425				430		
25	Gly	Met	Leu	Arg	Pro	Phe	Ala	Gly	Ile	Ala	Tyr	Asp	His	Ala	Gly	Ser
						435				440				445		
	Lys	Leu	Asp	Phe	Gly	Leu	Ser	Leu	Ser	Ala	Ala	Tyr	Arg	Met	Val	Leu
						450				455			460			
	Thr	His	Ser	Tyr	Lys	Ile	Arg	Thr	Ile	Gln	Lys	Glu	Gln	Leu	Asp	Tyr
30	465					470					475					480
	Gln	Leu	Ala	Tyr	Leu	Pro	Tyr	Ala	Tyr	Arg	Asn	Arg	Glu	Gly	Val	Glu
						485				490					495	
	Val	Arg	Ser	Ser	Leu	Tyr	Val	Ser	Ile	Pro	Met	Gln	Asn	Thr	His	Arg
						500				505				510		
35	Leu	Met	Thr	Glu	Leu	Arg	Leu	Tyr	Gly	Asp	Leu	Met	Lys	Arg	Lys	Asp
						515				520				525		

Gly Ile Ala Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser
 530 535 540
 Asp Pro Gln Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys
 545 550 555 560
 5 Asn Ile Ser Tyr Leu Phe
 565

(2) INFORMATION FOR SEQ ID NO:51

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...819

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

Arg Thr Asn Val Phe Leu Ser Leu Ser His Lys Ile Gly Arg Arg Gly
 1 5 10 15
 30 Ala Ser Cys Ser Asn Arg Asn Ala Trp Met Ala Glu Asn Lys Pro Ser
 20 25 30
 Ser Pro Glu Pro Asp Asn Thr Gly Val Gly Asn Ser Pro Ser Asp Tyr
 35 40 45
 Leu His Gly Glu Ala Ile Ile Pro Pro Leu Ser Ser Leu Ser Asn Phe
 35 50 55 60
 Asn Asp Lys Arg Phe Met Lys Lys Leu His Met Ile Ala Ala Leu Ala

	65		70		75		80									
	Val	Leu	Pro	Phe	Cys	Leu	Thr	Ala	Gln	Ala	Pro	Val	Ser	Asn	Ser	Glu
				85					90						95	
	Ile	Asp	Ser	Leu	Ser	Asn	Val	Gln	Leu	Gln	Thr	Val	Gln	Val	Val	Ala
5			100						105						110	
	Thr	Arg	Ala	Thr	Ala	Lys	Thr	Pro	Val	Ala	Tyr	Thr	Asn	Val	Arg	Lys
			115						120						125	
	Ala	Glu	Leu	Ser	Lys	Ser	Asn	Tyr	Gly	Arg	Asp	Ile	Pro	Tyr	Leu	Leu
		130					135						140			
10	Met	Leu	Thr	Pro	Ser	Val	Val	Ala	Thr	Ser	Asp	Ala	Gly	Thr	Gly	Ile
		145				150					155				160	
	Gly	Tyr	Ser	Gly	Phe	Arg	Val	Arg	Gly	Thr	Asp	Ala	Asn	Arg	Ile	Asn
				165						170					175	
	Ile	Thr	Thr	Asn	Gly	Val	Pro	Leu	Asn	Asp	Ser	Glu	Ser	Gln	Ser	Val
15			180						185					190		
	Phe	Trp	Val	Asn	Met	Pro	Asp	Phe	Ala	Ser	Ser	Ile	Glu	Asp	Leu	Gln
			195					200						205		
	Val	Gln	Arg	Gly	Val	Gly	Thr	Ser	Thr	Asn	Gly	Ala	Gly	Ala	Phe	Gly
		210					215						220			
20	Ala	Ser	Val	Asn	Met	Arg	Thr	Asp	Asn	Leu	Gly	Leu	Ala	Pro	Tyr	Gly
		225				230					235				240	
	Arg	Val	Asp	Leu	Ser	Gly	Gly	Ser	Phe	Gly	Thr	Phe	Arg	Arg	Ser	Val
				245						250					255	
	Lys	Leu	Gly	Ser	Gly	Arg	Ile	Gly	Arg	His	Trp	Ala	Val	Asp	Ala	Arg
25			260						265					270		
	Leu	Ser	Lys	Ile	Gly	Ser	Asp	Gly	Tyr	Val	Asp	Arg	Gly	Ser	Val	Asp
			275					280						285		
	Leu	Lys	Ser	Tyr	Phe	Ala	Gln	Val	Gly	Tyr	Phe	Gly	Ser	Asn	Thr	Ala
		290					295							300		
30	Leu	Arg	Phe	Ile	Thr	Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp
		305				310					315				320	
	Asn	Gly	Leu	Ser	Lys	Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn
				325						330					335	
	Ser	Ala	Gly	Leu	Met	Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr
35			340							345					350	
	His	Asn	Thr	Asp	Asn	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr

	355		360		365
	His Ser Phe Ser Pro Ser Val Ile Leu Asn Leu Thr Ala His Tyr Thr				
	370		375		380
	Ala Gly Tyr Gly Tyr Thr Asp Glu Tyr Arg Thr Gly Arg Lys Leu Lys				
5	385		390		395
	Glu Tyr Ala Leu Gln Pro Tyr Val Glu Asn Ser Val Thr Val Lys Lys				
		405		410	415
	Thr Asp Leu Ile Arg Gln Lys Tyr Leu Asp Asn Asp Phe Gly Gly Leu				
		420		425	430
10	Ile Gly Ser Leu Asn Trp His Thr Gly Ala Trp Asp Leu Gln Phe Gly				
		435		440	445
	Ala Ser Gly Asn Ile Tyr Lys Gly Asp His Phe Gly Arg Ile Thr Tyr				
		450		455	460
	Ile Lys Lys Tyr Asn Gln Pro Leu Ala Pro Asp Phe Glu Tyr Tyr Arg				
15	465		470		475
	Asn Arg Ala Asp Lys Arg Glu Gly Ala Ala Phe Ala Lys Ala Asn Trp				
		485		490	495
	Gln Ile Thr Pro Glu Leu Asn Met Tyr Ala Asp Leu Gln Tyr Arg Thr				
		500		505	510
20	Ile Gly Tyr Thr Ile Asn Gly Ile Thr Asp Glu Tyr Asp Glu Val Gln				
		515		520	525
	Gly Ser Met Gln His Ile Asp Leu Asp Lys Thr Phe Arg Phe Leu Asn				
		530		535	540
	Pro Lys Ala Gly Leu Thr Tyr Ser Phe Asp Asp Ala His Thr Ala Tyr				
25	545		550		555
	Ala Ser Val Ala Val Ala His Arg Glu Pro Asn Arg Thr Asn Tyr Thr				
		565		570	575
	Glu Ala Gly Ile Gly Gln Tyr Pro Thr Pro Glu Arg Leu Ile Asp Tyr				
		580		585	590
30	Glu Leu Gly Tyr Arg Tyr Ala Ser Pro Leu Leu Ser Ala Gly Val Gly				
		595		600	605
	Leu Tyr Tyr Met Gln Tyr Lys Asp Gln Leu Val Leu Asp Gly Arg Leu				
		610		615	620
	Ser Asp Val Gly Gln Met Leu Thr Ser Asn Val Pro Asp Ser Tyr Arg				
35	625		630		635
	Met Gly Leu Glu Leu Thr Leu Gly Trp Gln Ile Leu Pro Arg Leu Leu				

		645		650		655	
	Arg	Trp	Asp	Ala	Ser	Phe	Thr
				660			
	Val	Gln	Tyr	Thr	Ser	Val	Tyr
5			675			680	
	Lys	Glu	Glu	Thr	Leu	Glu	Ser
			690			695	
	Ile	Ala	Gly	Ser	Met	Leu	Thr
			705			710	
10	Trp	Thr	Ser	Arg	Phe	Val	Ser
				725			
	Ser	Asp	Arg	Met	Leu	Ser	Ser
				740			
	Tyr	Val	Leu	Pro	Val	His	Phe
15			755			760	
	Leu	Asn	Asn	Leu	Phe	Asn	Leu
			770			775	
	Asp	Ala	Gly	Tyr	Val	Gln	Ala
			785			790	
20	Leu	Arg	Tyr	Tyr	Pro	Gln	Ala
				805			
	Ile	Asp	Phe				

25 (2) INFORMATION FOR SEQ ID NO:52

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

5 (B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

```

Phe Thr Ser Gly Thr Ile Phe Val Arg Ile Ala Ile Ser Gly Arg Val
10 1          5          10          15
Val Cys Arg Glu Val Glu Asp Asn Gly Arg Arg Glu Ala Val Arg His
          20          25          30
Asp Gly Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val
          35          40          45
15 Val Arg Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val
          50          55          60
Ser Ala Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys
65          70          75          80
Asp Thr Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg
20          85          90          95
Val Ala Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His
          100          105          110
Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly
          115          120          125
25 Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg
          130          135          140
Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile
145          150          155          160
Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys
30          165          170          175
Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys
          180          185          190
Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly
          195          200          205
35 Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp
          210          215          220

```

15

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

30

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

35

Ser Thr Ile Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu
1 5 10 15
Gly Leu Cys Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly

	20		25		30
	His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr				
	35		40		45
	Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile				
5	50		55		60
	Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile				
	65		70		75
	Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu				
	85		90		95
10	Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu				
	100		105		110
	Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe				
	115		120		125
	Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr				
15	130		135		140
	Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu				
	145		150		155
	Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro				
	165		170		175
20	Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser				
	180		185		190
	Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys				
	195		200		205
	Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe				
25	210		215		220
	Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp				
	225		230		235
	Thr Phe Asn				240

30

(2) INFORMATION FOR SEQ ID NO:54

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

10

(A) NAME/KEY: misc_feature

(B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

```

15  Trp Cys Gln Ser Asp Pro Ile Pro His Cys His Ala Val Tyr Arg Asn
    1           5           10           15
    Ala Gln Gly His Gln Gln Gly Arg Ser Asp Gln Asp Arg Leu Pro Pro
        20           25           30
    Val Arg Gly Tyr Arg Tyr Ala Arg Cys Leu Gly Arg Tyr Glu Gly Phe
20          35           40           45
    Gly Glu Arg Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met
        50           55           60
    Leu Pro Ala Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu
        65           70           75           80
25  Arg Leu Glu Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile
        85           90           95
    Arg Ser Ala Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val
        100          105          110
    Lys Gly Tyr Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr
30          115          120          125
    Ser Leu Pro Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr
        130          135          140
    Leu Asn Tyr Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser
        145          150          155          160
35  Asp Leu Pro Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile
        165          170          175

```

[illegible]

(2) INFORMATION FOR SEQ ID NO:55

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 447 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...447

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

Pro Phe Ser Pro Pro Trp Val Cys Ala Gly Ala Ala Ser Ser Val Arg
 1 5 10 15
 Thr Arg Pro Cys Ser Thr Val Ser Ser Thr Ala Ala Ser Ser His Arg
 25 20 25 30
 Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro
 35 40 45
 Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln
 50 55 60
 30 Arg Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly
 65 70 75 80
 Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu
 85 90 95
 Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys
 35 100 105 110
 Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val

	115		120		125	
	Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met					
	130		135		140	
	Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln					
5	145		150		155	160
	Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser					
		165		170		175
	Asn Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val					
		180		185		190
10	Ser Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr					
		195		200		205
	Asp Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr					
		210		215		220
	Met Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro					
15	225		230		235	240
	Glu Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe					
		245		250		255
	Ala Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr					
		260		265		270
20	Pro Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala					
		275		280		285
	Leu His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg					
		290		295		300
	Asn Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg					
25	305		310		315	320
	Ile Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp					
		325		330		335
	Lys Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp					
		340		345		350
30	Val Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp					
		355		360		365
	Gln Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro					
		370		375		380
	Ala Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met					
35	385		390		395	400
	Gly Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val					

	405	410	415
	Thr Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser		
	420	425	430
	Thr Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu		
5	435	440	445

(2) INFORMATION FOR SEQ ID NO:56

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 532 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...532

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

	Tyr	Arg	Arg	Ser	Gly	Arg	Val	Cys	Pro	Arg	Ile	Leu	Arg	Asn	Lys	Arg
1					5					10					15	
	Ser	Tyr	Ala	Asp	Thr	Arg	Leu	Gln	Pro	Arg	Arg	Ala	Val	Arg	Leu	Arg
30				20					25					30		
	Ala	Gly	Thr	Arg	Thr	Lys	Met	Lys	Arg	Arg	Phe	Leu	Ser	Leu	Leu	Leu
				35				40					45			
	Leu	Tyr	Ile	Leu	Ser	Ser	Ile	Ser	Leu	Ser	Ala	Gln	Arg	Phe	Pro	Met
				50			55				60					
35	Val	Gln	Gly	Ile	Glu	Leu	Asp	Thr	Asp	Ser	Leu	Phe	Ser	Leu	Pro	Lys
	65					70					75				80	

	Arg	Pro	Trp	Arg	Ala	Ile	Gly	Lys	Thr	Ile	Gly	Val	Asn	Leu	Ala	Val	
					85					90					95		
	Trp	Gly	Phe	Asp	His	Phe	Ile	Met	Asn	Glu	Asp	Phe	Ala	Asp	Ile	Ser	
				100					105					110			
5	Trp	Gln	Thr	Ile	Lys	Ser	Asn	Phe	Gln	Thr	Gly	Phe	Gly	Trp	Asp	Asn	
			115					120					125				
	Asp	Lys	Phe	Val	Thr	Asn	Leu	Phe	Ala	His	Pro	Tyr	His	Gly	Ser	Leu	
			130					135					140				
	Tyr	Phe	Asn	Ala	Ala	Arg	Ser	Asn	Gly	Leu	Ser	Phe	Arg	His	Ser	Ala	
10	145					150					155				160		
	Pro	Phe	Ala	Phe	Phe	Gly	Ser	Leu	Met	Trp	Glu	Leu	Leu	Met	Glu	Asn	
					165					170					175		
	Glu	Pro	Pro	Ser	Ile	Asn	Asp	Leu	Cys	Ala	Thr	Thr	Ile	Gly	Gly	Ile	
				180					185					190			
15	Ala	Leu	Gly	Glu	Met	Gly	His	Arg	Leu	Ser	Asp	Leu	Leu	Ile	Asp	Asn	
			195					200					205				
	Arg	Thr	Thr	Gly	Trp	Glu	Arg	Met	Gly	Arg	Glu	Val	Ala	Ile	Ala	Leu	
			210					215					220				
	Ile	Asn	Pro	Met	Arg	Phe	Leu	Asn	Arg	Leu	Thr	Ala	Gly	Glu	Val	Thr	
20	225					230					235				240		
	Ser	Val	Gly	Ser	Arg	Ser	Gly	Gln	Ile	Phe	Gln	Ser	Val	Pro	Ile	Asn	
				245						250					255		
	Ile	Val	Val	Asp	Ala	Gly	Phe	Arg	Phe	Leu	Ala	Asp	Lys	Arg	His	Ala	
				260					265					270			
25	Arg	Thr	Gly	Ala	Thr	Ala	Leu	Thr	Leu	Asn	Leu	Arg	Phe	Asp	Tyr	Gly	
			275					280					285				
	Asp	Pro	Phe	Arg	Ser	Glu	Thr	Phe	Ser	Pro	Tyr	Asp	Phe	Phe	Gln	Phe	
			290					295					300				
	Lys	Ala	Gly	Leu	Ser	Phe	Ser	Glu	Ser	Gln	Pro	Leu	Leu	Ser	Gln	Ile	
30	305					310					315				320		
	Asn	Leu	Ile	Gly	Ile	Leu	Ser	Gly	Cys	Gln	Leu	Leu	Ala	His	Glu	Arg	
				325						330					335		
	Thr	Val	Leu	Val	Gly	Gly	Leu	Phe	Gln	His	Phe	Asp	Tyr	Tyr	Asn	Ser	
				340					345					350			
35	Glu	Lys	Arg	Ile	Ser	Lys	Asn	Ser	Glu	Glu	Val	Leu	Val	Thr	Pro	Tyr	
			355					360						365			

Arg Ile Ser Gln Val Ala Ala Leu Gly Gly Gly Leu Ile Phe Gln His
 370 375 380
 His Gly Lys Phe Arg Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr
 385 390 395 400
 5 Leu Asn Val Val Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val
 405 410 415
 Asp Asn Arg Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr
 420 425 430
 Leu Gly Ala Thr Tyr Asn Asp Leu Trp Ser Trp Leu Leu Gly Val Glu
 10 435 440 445
 Ser Tyr Arg Leu Tyr Thr Trp Ile Gly Tyr Glu Glu Pro His Gln Lys
 450 455 460
 Asn Thr Asp Val Ser Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala
 465 470 475 480
 15 Arg Leu Leu Val Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp
 485 490 495
 His Val Ala Ile Val Ala Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln
 500 505 510
 Phe Tyr Pro Asn Val Ser Phe Asp Thr Gly Asp Ile Gln Leu Arg Val
 20 515 520 525
 Gly Phe His Phe
 530

(2) INFORMATION FOR SEQ ID NO:57

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

```

Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met
1           5           10           15
10 Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala
    20           25           30
    Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu
    35           40           45
    Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn
15      50           55           60
    Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys
    65           70           75           80
    Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr
    85           90           95
20 Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu
    100          105          110
    Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala
    115          120          125
    Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser
25      130          135          140
    Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala
    145          150          155          160
    Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe
    165          170          175
30 Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp
    180          185          190
    Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys
    195          200          205
    Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn
35      210          215          220
    Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala

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225 230 235 240
 Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu
 245 250 255
 Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu
 5 260 265 270
 Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe
 275 280 285
 Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe
 290 295 300
 10

(2) INFORMATION FOR SEQ ID NO:58

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 973 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

25 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

30
 Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu
 1 5 10 15
 Phe Pro Leu Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys
 20 25 30
 35 Lys Glu Lys His Ser Val Thr Glu Ile Ala Unk Glu Lys Lys Arg Ile
 35 40 45

	Thr	Ala	Leu	Leu	Tyr	Glu	Lys	Glu	Leu	Pro	Thr	Asp	Ser	Val	Lys	Gln
	50						55					60				
	Leu	Tyr	Glu	Asn	Ser	Val	Gln	Asn	Lys	Asn	Leu	Val	Gly	Gln	Met	Leu
	65					70				75					80	
5	Phe	Ala	Ile	Glu	Val	Gly	Lys	Arg	Met	Arg	Asn	Met	Ser	Gln	Tyr	Thr
					85					90				95		
	Asp	Ala	Met	Leu	Tyr	His	Gln	Lys	Gly	Leu	Asn	Ala	Ala	Leu	Asn	Leu
				100					105					110		
	Arg	Asp	Thr	Ile	Val	Ala	Ala	Gln	Ala	Trp	Asn	His	Leu	Gly	Thr	Asp
10			115					120					125			
	Ser	Arg	Arg	Ile	Gly	Ala	Leu	Ala	Glu	Ala	Ser	Asp	Tyr	His	Tyr	Lys
		130					135					140				
	Ala	Leu	Ser	Leu	Ile	Glu	Ser	Phe	Ser	Gly	Asn	Gln	Asn	Arg	Pro	Ala
	145				150				155					160		
15	Ile	Lys	Ala	Arg	Ser	Ala	Ala	Leu	Asn	Gly	Ile	Gly	Asn	Ile	Asn	Leu
				165					170					175		
	Glu	Leu	Gly	Tyr	His	Asp	Glu	Ala	Glu	Lys	Asn	Phe	Leu	Lys	Ala	Leu
				180				185					190			
	Gln	Gly	Glu	Lys	Glu	Leu	Asp	Ser	Pro	Leu	Gly	Gln	Ala	Ile	Asn	Tyr
20			195					200					205			
	Ala	Asn	Leu	Gly	Arg	Ile	Tyr	Arg	Gln	Arg	Lys	Glu	Tyr	Asp	Lys	Ala
		210				215					220					
	Arg	Thr	Tyr	Phe	Leu	Leu	Ser	Leu	Glu	Gln	Asn	Asn	Met	Ala	Glu	Asn
	225				230				235						240	
25	Leu	Met	Gly	Ile	Gly	Leu	Cys	Ser	Ile	Asn	Leu	Gly	Glu	Val	Asp	Glu
				245					250					255		
	Glu	Lys	Gly	Asp	Tyr	Gln	Lys	Ala	Leu	Gln	Glu	Tyr	Ala	Thr	Ala	Tyr
			260					265					270			
	Lys	Leu	Met	Glu	Gln	Leu	Ser	Asp	Arg	Trp	His	Trp	Leu	Asn	Ser	Cys
30			275					280					285			
	Ile	Pro	Met	Ala	Arg	Ile	Asn	Leu	Lys	Gln	Gly	Asn	Glu	Arg	Leu	Tyr
		290				295					300					
	Gln	His	Phe	Ile	Ser	Leu	Ala	Glu	Gly	Thr	Ala	Lys	Glu	Ile	Asn	Ser
	305				310				315					320		
35	Thr	Ser	His	Leu	Ile	Glu	Ile	Tyr	Asn	Leu	Gln	Tyr	Glu	Asn	Leu	Glu
				325					330					335		

	Arg	Lys	Lys	Glu	Tyr	Lys	Gln	Ala	Leu	Glu	Ala	Phe	Cys	Leu	Ser	Lys	
				340					345						350		
	Thr	Leu	Ser	Asp	Ser	Met	Ser	Ile	Ala	His	Lys	Val	Ser	Ser	Ile	Gln	
			355					360					365				
5	Glu	Thr	Arg	Phe	Asn	Tyr	Glu	Arg	Asn	Lys	Ser	Gln	Lys	Glu	Leu	Glu	
		370					375					380					
	Glu	Ile	Gln	Gln	Val	Ser	Lys	Ala	Lys	Gln	Glu	Lys	Ser	Lys	Phe	Ile	
	385					390					395				400		
	Leu	Leu	Ser	Thr	Leu	Phe	Ala	Leu	Phe	Ile	Ser	Ile	Leu	Leu	Ile	Ser	
10					405					410					415		
	Val	Leu	Thr	Tyr	Ala	Tyr	Arg	Gln	Gly	Lys	Lys	His	Asn	Lys	Leu	Ile	
				420					425					430			
	Lys	Glu	Thr	Asp	Lys	Leu	Arg	Ser	Gly	Phe	Phe	Thr	Gly	Ile	Thr	His	
		435					440					445					
15	Glu	Phe	Arg	Thr	Pro	Ile	Thr	Val	Ile	Gln	Gly	Leu	Asn	Glu	Lys	Met	
		450				455					460						
	Ser	Ser	Ser	Pro	Asp	Leu	Gln	Ala	Ser	Asp	Arg	Thr	Glu	Leu	His	Lys	
	465					470				475					480		
	Ile	Ile	Asp	Arg	Gln	Ser	Ser	His	Met	Leu	Asn	Leu	Val	Asn	Gln	Leu	
20				485					490					495			
	Leu	Asp	Ile	Cys	Lys	Ile	Arg	Ser	Gly	Val	Ser	Thr	Pro	Glu	Trp	Arg	
			500						505					510			
	Asn	Gly	Asp	Ile	Val	Ser	Phe	Val	Gln	Ile	Leu	Ile	Asp	Ser	Phe	Ala	
		515						520					525				
25	Pro	Tyr	Ala	Gln	Ala	Gln	Asp	Ile	Thr	Leu	Glu	Leu	Gln	Pro	Glu	Ser	
		530				535						540					
	Lys	Pro	Ile	Val	Val	Asp	Phe	Val	Pro	Ser	Tyr	Leu	Gln	Lys	Ile	Ile	
	545					550				555					560		
	Ser	Asn	Leu	Leu	Ser	Asn	Ala	Ile	Lys	Tyr	Ser	Leu	Ala	Gly	Gly	Arg	
30				565					570					575			
	Val	Val	Ile	Ser	Leu	Ala	Lys	Thr	Lys	Asn	Glu	Lys	Asn	Leu	Ile	Ile	
			580						585					590			
	Arg	Val	Ala	Asp	Asn	Gly	Ile	Gly	Ile	Asp	Lys	Thr	Asp	Gln	Ala	His	
		595						600					605				
35	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr	Glu	Lys	His	Gly	
		610					615						620				

	Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val Glu Asn Leu Arg	
	625	630 635 640
	Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly Ser Ala Phe Thr	
		645 650 655
5	Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala Glu Ile Leu Pro	
		660 665 670
	Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val His Ile Ala Pro	
		675 680 685
	Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu Asn His Arg Phe	
10		690 695 700
	Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp Asn Lys Asp Ile	
		705 710 715 720
	Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr Asn Val Leu Ser	
		725 730 735
15	Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr Glu His Ile Pro	
		740 745 750
	Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met Asp Gly Ile Glu	
		755 760 765
	Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys His Ile Pro Ile	
20		770 775 780
	Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg Leu Glu Gly Ile	
		785 790 795 800
	Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe Ser Pro Glu Glu	
		805 810 815
25	Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg Glu Leu Leu Lys	
		820 825 830
	Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys Pro Glu Glu Glu	
		835 840 845
	Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu Leu Ala Ala Lys	
30		850 855 860
	Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp Phe Ser Ala Gln	
		865 870 875 880
	Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln Leu Asn Arg Lys	
		885 890 895
35	Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr Ile Gln Gln Ile	
		900 905 910

Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu Ser Lys Asn Ile
 915 920 925
 Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro Ala Tyr Phe Ser
 930 935 940
 5 Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser Gln Tyr Arg Gln
 945 950 955 960
 Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr Val
 965 970

10 (2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- 25 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

30 Tyr Lys Gln Ala Ile Met Lys His Leu Phe Lys Ser Thr Leu Val Leu
 1 5 10 15
 Leu Cys Ala Leu Ser Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn
 20 25 30
 Asn Thr Glu Lys Ser Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly
 35 35 40 45
 Tyr Ile Ala Gly Ser Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala

50 55 60
 Asn Asp Arg Leu Leu Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser
 65 70 75 80
 Lys Lys Glu Asn Ala Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser
 5 85 90 95
 Pro Gly Tyr Tyr Val Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr
 100 105 110
 Ala Phe Tyr Val Val Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg
 115 120 125
 10 Pro Ile Lys Asn Phe Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala
 130 135 140
 Trp Met Ser Arg His Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp
 145 150 155 160
 Asp Lys Gln Arg Lys Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met
 15 165 170 175
 His Leu Gln Unk His Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr
 180 185 190
 Asp Leu Thr Ser Cys Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln
 195 200 205
 20 Lys Asp Arg Thr Phe Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly
 210 215 220
 Leu Asn Leu
 225

25 (2) INFORMATION FOR SEQ ID NO:60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

5 (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

	Met	Lys	Thr	Ile	Ser	Lys	Asn	His	Ala	Ala	Arg	Ile	Cys	Ala	Ala	Ile
10	1				5					10					15	
	Ala	Leu	Phe	Ala	Val	Cys	Asn	Gly	Arg	Ile	Ala	Ala	Gln	Asp	Phe	Leu
				20					25					30		
	Tyr	Glu	Ile	Gly	Gly	Gly	Phe	Gly	Ala	Ala	Gln	Tyr	Phe	Gly	Asp	Ala
			35					40					45			
15	Asn	Arg	Gly	Leu	Phe	Gly	Ser	Ser	Gly	Val	Gly	Leu	Glu	Leu	Val	Gly
		50					55				60					
	Arg	Tyr	Asn	Tyr	Asn	Phe	Arg	Trp	Ala	Phe	Ser	Thr	Met	Leu	Asp	Trp
	65				70					75					80	
	Arg	Thr	Leu	Arg	Gly	Asp	Thr	Asp	Lys	Ser	Gly	Asn	Val	Phe	Pro	Asp
20				85					90					95		
	Phe	Ala	Gln	Ala	Asp	Phe	Lys	Val	Gly	Leu	Thr	Gln	Leu	His	Val	Arg
			100						105					110		
	Ser	Glu	Phe	Asn	Phe	Leu	Pro	Tyr	Ser	Asp	Gly	Tyr	Lys	Tyr	Leu	Gly
			115					120					125			
25	Thr	Ala	Arg	Leu	Ser	Pro	Tyr	Val	Ala	Ala	Gly	Leu	Ser	Leu	Gly	Phe
		130					135					140				
	Ala	Ser	Gly	Ala	Lys	Gly	Ser	Ala	Phe	Ala	Pro	Gly	Ile	Thr	Ala	Gly
	145				150					155				160		
	Met	Gly	Val	Lys	Tyr	Lys	Leu	Lys	Pro	Arg	Ile	Asn	Val	Gly	Ile	Glu
30				165					170					175		
	Tyr	Ser	Phe	Thr	Gly	Leu	Leu	Thr	Asp	Ala	Leu	Asp	Ala	Leu	Thr	Asp
			180					185					190			
	Lys	Ser	Val	Trp	Leu	Glu	Asp	Pro	Tyr	Lys	Ile	Asn	Asp	Ser	Trp	Val
			195				200						205			
35	Lys	Asn	Lys	Asp	Ala	Thr	Gly	Ala	Leu	Val	Leu	Arg	Ile	Thr	Tyr	Asp
		210					215					220				

Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln
 225 230 235

(2) INFORMATION FOR SEQ ID NO:61

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1162

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

	Ala	Ile	Ser	Gln	Met	Lys	Arg	Ile	Leu	Pro	Ile	Val	Ala	Phe	Leu	Ser
25	1				5					10					15	
	Leu	Phe	Leu	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Gln	Arg	Ala	Met	Gly
				20					25					30		
	Lys	Thr	Ala	Asp	Arg	Ser	Leu	Met	Ala	Ser	Gly	His	Trp	Val	Lys	Ile
			35				40					45				
30	Arg	Val	Asp	Ala	Ser	Gly	Val	Tyr	Arg	Leu	Thr	Asp	Glu	Gln	Leu	Arg
		50				55					60					
	Ala	Asn	Gly	Phe	Ser	Asp	Pro	Ser	Lys	Val	Gly	Val	Phe	Gly	Tyr	Gly
	65				70				75					80		
	Gly	Gly	Val	Leu	Pro	Glu	Asp	Leu	Ser	Arg	Ile	Thr	Thr	Asp	Asp	Leu
35				85					90					95		
	Pro	Pro	Val	Pro	Val	Leu	Arg	Gln	Gly	Asn	Ala	Leu	Tyr	Phe	Tyr	Ala

	100	105	110
	Val Gly Pro Val Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu		
	115	120	125
	His Thr Val Asn Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp		
5	130	135	140
	Ala Ala Gly Ala Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala		
	145	150	155
	Ser Ala Glu Ala Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu		
	165	170	175
10	Gln Glu Leu Tyr Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu		
	180	185	190
	Ser Phe Ser Ala Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly		
	195	200	205
	Asn Thr Arg Ser Ser Gly Glu Leu Gly Thr Val Phe Ser Tyr Ile Ala		
15	210	215	220
	Lys Ala Arg Ser Ala Gly Gly Gly Arg Glu Met Ser Leu Ser Ala Asn		
	225	230	235
	Gly Ile Leu Ile Phe Ser Asp Pro Phe Ser Met Thr Ser Asn Glu Val		
	245	250	255
20	Ser Asn Ser Tyr Leu Ala Gly Lys Lys Arg Arg Leu Tyr His Ser Thr		
	260	265	270
	Pro Met Asn Ser Leu Val Asn Glu Leu Arg Leu Asp Ala Asn Tyr Ser		
	275	280	285
	Met Thr Gly Asp Ala Val Asn Leu Asp Phe Ile Glu Val Ala Thr Gln		
25	290	295	300
	Asn Asp Leu Arg Tyr Asp Gly Ala Pro Met His Ile Arg Arg Phe Ser		
	305	310	315
	Asn Leu Pro Val Leu Gly Gly Glu Ser Cys Arg Phe Val Ile Ser Glu		
	325	330	335
30	Val Pro Glu Ser Leu Val Val Leu Gln Ala Asn Ser Ser Leu Thr Ala		
	340	345	350
	Ser Leu Val Pro Val Lys Thr Val Gly Asp Lys Thr Ile Glu Phe Val		
	355	360	365
	Ala Pro Pro Lys Gly Gln Asp Arg Arg Thr Ile Asn Thr Phe Tyr Ala		
35	370	375	380
	Val Asp Leu Ser Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro		

	385		390		395		400									
	Asn	Gln	Asn	Leu	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser
			405						410						415	
	Thr	Gln	Ala	Leu	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg
5			420						425						430	
	Glu	Lys	Asn	Gly	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe
			435						440					445		
	Asn	Glu	Phe	Ser	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe
			450						455					460		
10	Ala	Lys	Met	Phe	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu
			465						470					475		480
	Thr	Phe	Pro	Met	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn
					485					490					495	
	Arg	Lys	Val	Ser	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu
15			500						505					510		
	Phe	Leu	Leu	Thr	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr
			515						520					525		
	Val	Thr	Asp	Asp	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val
			530						535					540		
20	Asn	Ile	Gly	Trp	Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val
			545						550					555		560
	Arg	Thr	Pro	Ala	Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr
					565					570					575	
	Glu	Glu	Asp	Arg	Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala
25			580						585					590		
	Ala	Asp	Asn	Gly	Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp
			595						600					605		
	Thr	Val	Lys	Arg	Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln
			610						615					620		
30	Asp	Val	Tyr	Pro	His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly
			625						630					635		640
	Ala	Lys	Lys	Lys	Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu
					645					650					655	
	Asn	Tyr	Ala	Gly	His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu
35			660							665				670		
	Leu	Thr	Leu	Asn	Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile

	675		680		685
	Trp Ile Thr Ala Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr				
	690		695		700
	Ser Ala Gly Glu Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile				
5	705		710		715 720
	Met Phe Ser Thr Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile				
		725		730	735
	Asn Gly Phe Met Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg				
		740		745	750
10	Tyr Arg Thr Met Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu				
		755		760	765
	Ser Thr Val Phe Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met				
		770		775	780
	Gly Asp Pro Ser Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu				
15	785		790		795 800
	Thr Ala Ile Asn Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met				
		805		810	815
	Leu Lys Ser Leu Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu				
		820		825	830
20	Lys Gly Thr Phe Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val				
		835		840	845
	Phe Asp Gly Arg Lys Lys Met Thr Ala Leu Glu Glu Glu Gly Asn Asp				
		850		855	860
	Leu Ser Leu Val Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile				
25	865		870		875 880
	Ala Glu Val Lys Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys				
		885		890	895
	Asp Val Asn Tyr Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr				
		900		905	910
30	Asn Glu Ser Thr Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg				
		915		920	925
	Val Gln Pro Gly Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro				
		930		935	940
	Glu Ile Ile Ser Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp				
35	945		950		955 960
	Glu Val Asn Pro Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn				

	965	970	975
	Gly Ile Asn Ile Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys		
	980	985	990
	Ile Asp Gly Arg Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr		
5	995	1000	1005
	Ser Ser Ala Thr Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro		
	1010	1015	1020
	Ala Leu Ala Glu Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile		
	1025	1030	1035
10	Phe Asn Asn Ala Val His His Asp Phe Ser Phe Arg Val Val Asp Gly		
	1045	1050	1055
	Ile Ala Pro Asp Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg		
	1060	1065	1070
	Glu Ser Ala Thr Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu		
15	1075	1080	1085
	Asn Val Ala Val Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser		
	1090	1095	1100
	Leu Pro Val Lys Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile		
	1105	1110	1115
20	Lys Trp Asp Leu Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe		
	1125	1130	1135
	Tyr Leu Tyr Arg Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser		
	1140	1145	1150
	Met Ala Lys Lys Met Ile Val Val Gly Gln		
25	1155	1160	

(2) INFORMATION FOR SEQ ID NO:62

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 406 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

10

```

Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met
1           5           10           15
Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu
           20           25           30
15 Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val
           35           40           45
Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala
           50           55           60
Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser
20 65           70           75           80
Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly
           85           90           95
Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile
           100          105          110
25 Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn
           115          120          125
Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu
           130          135          140
Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu
30 145          150          155          160
Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser
           165          170          175
Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn
           180          185          190
35 Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly
           195          200          205

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Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser
 210 215 220
 Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly
 225 230 235 240
 5 Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly
 245 250 255
 Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu
 260 265 270
 Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn Asp
 10 275 280 285
 Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser
 290 295 300
 Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys
 305 310 315 320
 15 Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr
 325 330 335
 Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr
 340 345 350
 Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn
 20 355 360 365
 Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn
 370 375 380
 Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly
 385 390 395 400
 25 Leu Arg Asn Leu Phe His
 405

(2) INFORMATION FOR SEQ ID NO:63

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...221

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

```

Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg
1           5           10           15
Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile
15          20          25          30
Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn
          35          40          45
Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn
          50          55          60
20 Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala
65          70          75          80
Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met
          85          90          95
Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His
25          100         105         110
Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp
          115         120         125
Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val
          130         135         140
30 Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp
145         150         155         160
Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu
          165         170         175
Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu
35          180         185         190
His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu

```

195 200 205
 Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
 210 215 220

5 (2) INFORMATION FOR SEQ ID NO:64

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

20 (A) NAME/KEY: misc_feature

(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

25 Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr
 1 5 10 15
 Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg
 20 25 30
 Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met Ser Gly Leu Ser
 30 35 40 45
 Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn Leu Asn Leu Arg
 50 55 60
 Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser Leu Asp Ala Ala
 65 70 75 80
 35 Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile Gly His Asn Tyr
 85 90 95

Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr Val Asp Arg Ser
 100 105 110
 Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val Glu Val Phe Ser
 115 120 125
 5 Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys Tyr Asn Val Glu
 130 135 140
 Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp Leu Ser Leu Gln
 145 150 155 160
 Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln Glu Met Thr Arg
 10 165 170 175
 Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln Arg Asn Arg Thr
 180 185 190
 Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly Lys Leu Leu Asp
 195 200 205
 15 Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu Val Gln Tyr Arg
 210 215 220
 Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln Ala Leu Glu Leu
 225 230 235 240
 Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp Thr Asp Val Leu
 20 245 250 255
 Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu Glu Ile Tyr Arg
 260 265 270
 Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser Glu Leu Gln Ile
 275 280 285
 25 Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala Ala Tyr Phe Pro
 290 295 300
 Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr Phe Arg Asp Leu
 305 310 315 320
 Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser Glu Gln Trp Lys
 30 325 330 335
 Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn Ile Pro Ile Phe
 340 345 350
 Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser Arg Leu Gln Ile
 355 360 365
 35 Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys Ala Leu Tyr Lys
 370 375 380

Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala Asp Lys Ala Ile
 385 390 395 400
 Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys Ala Tyr Glu Tyr
 405 410 415
 5 Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala Tyr Glu Tyr Ala
 420 425 430
 Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu Glu Leu Arg Ala
 435 440 445
 Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp Phe Tyr Gln Gly
 10 450 455 460
 Lys Asp Phe
 465

(2) INFORMATION FOR SEQ ID NO:65

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

30

(B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp
 35 1 5 10 15
 Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala

	20		25		30
	Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly				
	35		40		45
	Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu				
5	50		55		60
	Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala				
	65		70		75
	Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala				
		85		90	
10	Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg				
	100		105		110
	Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys				
	115		120		125
	Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr				
15	130		135		140
	Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr				
	145		150		155
	Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile				
		165		170	
20	Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser				
	180		185		190
	Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu				
	195		200		205
	Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala				
25	210		215		220
	Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg				
	225		230		235
	Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser				
		245		250	
30	Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu				
	260		265		270
	Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro				
	275		280		285
	His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu				
35	290		295		300
	Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr				

305 310 315 320
 Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly
 325 330 335
 Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg
 5 340 345 350
 Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr
 355 360 365
 Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly
 370 375 380
 10 Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu
 385 390 395 400
 Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala
 405 410 415
 Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys
 15 420 425 430
 Leu Lys Leu Asn
 435

(2) INFORMATION FOR SEQ ID NO:66

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...945

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

```

Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln
1           5           10           15
5  Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu
    20           25           30
Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala
    35           40           45
Gly Arg Val Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val
10      50           55           60
Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr
65           70           75           80
Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr
    85           90           95
15  Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile
    100          105          110
Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn
    115          120          125
Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala
20      130          135          140
Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr
145          150          155          160
Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro
    165          170          175
25  Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp
    180          185          190
Ile Ser Lys Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro
    195          200          205
Gln Val Ala Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln
30      210          215          220
Val Leu Asn Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp
225          230          235          240
Gly Glu Glu Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys
    245          250          255
35  Lys Gly Leu Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg
    260          265          270

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	Tyr Met Ala Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp	
	275	280 285
	Thr Leu Ile Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu	
	290	295 300
5	Met Asp Ser Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly	
	305	310 315 320
	Gly Arg Arg Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met	
		325 330 335
	Leu Gly Gly Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly	
10		340 345 350
	Gly Asp Ala Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys	
		355 360 365
	Arg Val Glu Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn	
		370 375 380
15	Ile Leu Glu Arg Ser Phe Ser His Asn Gly Gln Ala Arg Phe Arg Met	
		385 390 395 400
	Gln Trp Lys Pro Ser Glu Arg Thr Glu Val Val Phe Glu Pro Asp Leu	
		405 410 415
	Ser Ile Ser Lys Ile Asp Gly Phe Phe Asn Asp Thr Tyr Glu Thr Lys	
20		420 425 430
	Asp Ala Thr Gly Ile Ser Ile Asn Lys Gly Ser Ile His Gln Thr Thr	
		435 440 445
	Gln Gly Asn Asn Phe Arg Leu Asn Gly Glu Leu Asp Ile Ser His Lys	
		450 455 460
25	Leu Asn Asp Glu Gly Arg Thr Ile Ser Ala Ser Val Ser Gly Gly Leu	
		465 470 475 480
	Thr Asp Glu Asp Gly Asp Gly Ile Tyr Gln Ala Val Leu Gln Ser Val	
		485 490 495
	Glu Thr Asn Gln Lys Gln Phe Asn Asp Asn Ser Asn Leu Gln Tyr Arg	
30		500 505 510
	Leu Arg Leu Ser Tyr Val Glu Pro Leu Gly Lys Asn Tyr Phe Ala Gln	
		515 520 525
	Ala Ile Leu Asn Arg Arg Phe Ser Arg Arg Asn Ser Asp Arg Glu Val	
		530 535 540
35	Tyr Arg Leu Gly Asp Asp Gly Gln Tyr Ser Ile Leu Asp Ser Gln Tyr	
		545 550 555 560

	Gly	Leu	Ser	Tyr	Ser	Asn	Glu	Phe	Thr	Gln	Tyr	Arg	Ile	Gly	Leu	Asn	
						565					570				575		
	Leu	Lys	Lys	Ile	Ala	Lys	Thr	Trp	Asp	Tyr	Thr	Val	Gly	Phe	Asn	Val	
						580					585				590		
5	Asp	Pro	Asn	Arg	Thr	Val	Ser	Tyr	Arg	Ser	Val	Ala	Gly	Val	Glu	Gln	
						595					600				605		
	Asp	Lys	Leu	Ala	Phe	Asn	Arg	Val	Asn	Leu	Ser	Pro	Met	Leu	Arg	Ile	
						610					615				620		
	Asn	Tyr	Lys	Pro	Ser	Arg	Thr	Thr	Asn	Leu	Arg	Val	Asp	Tyr	Arg	Gly	
10	625					630					635				640		
	Arg	Thr	Thr	Gln	Pro	Ser	Ile	Asn	Gln	Ile	Ala	Pro	Val	Gln	Asp	Ile	
						645					650				655		
	Thr	Asn	Pro	Leu	Phe	Val	Thr	Glu	Gly	Asn	Pro	Gly	Leu	Lys	Pro	Ser	
						660					665				670		
15	Tyr	Ser	Asn	Asn	Val	Met	Ala	Met	Phe	Ser	Asp	Phe	Asp	Ala	Lys	Ser	
						675					680				685		
	Gln	Arg	Ala	Phe	Asn	Ile	Val	Phe	Phe	Gly	Asn	Tyr	Thr	Phe	Asp	Asp	
						690					695				700		
	Ile	Val	Pro	Asn	Thr	His	Tyr	Asp	Pro	Ser	Thr	Gly	Ile	Arg	Thr	Thr	
20	705					710					715				720		
	Arg	Tyr	Glu	Asn	Ala	Ser	Gly	Thr	Trp	Gln	Ala	Asn	Leu	His	Gly	Thr	
						725					730				735		
	Leu	Ser	Leu	Pro	Leu	Lys	Asn	Arg	Ala	Phe	Ser	Phe	Arg	Met	Ser	Leu	
						740					745				750		
25	Phe	Asn	Arg	Leu	Ala	Glu	Gly	Gln	Ser	Phe	Ile	Asn	Asp	Asp	Lys	Asn	
						755					760				765		
	Lys	Ala	Leu	Ser	Phe	Arg	Thr	Arg	Glu	Arg	Leu	Thr	Leu	Thr	Tyr	Arg	
						770					775				780		
	Asn	Asn	Trp	Ile	Asp	Thr	Ser	Ile	Gly	Gly	Asn	Ile	Gly	Phe	Tyr	Met	
30	785					790					795				800		
	Ala	Asn	Asn	Ser	Leu	Ser	Gly	Gln	Lys	Asp	Ser	Arg	Thr	Tyr	Asp	Phe	
						805					810				815		
	Gly	Gly	Asn	Tyr	Gln	Val	Ala	Leu	Thr	Leu	Pro	Tyr	Gly	Phe	Arg	Ile	
						820					825				830		
35	Asp	Ser	Asp	Val	Glu	Tyr	Asn	Thr	Asn	Ser	Gly	Tyr	Ser	Gly	Gly	Phe	
						835					840				845		

Ser Leu Asp Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu
 850 855 860
 Arg Asp Lys Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly
 865 870 875 880
 5 Gln Arg Ser Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu
 885 890 895
 Ser Met Ser Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr
 900 905 910
 Arg Phe Asn Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg
 10 915 920 925
 Gly Asn Met Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro
 930 935 940
 Ser
 945

15

(2) INFORMATION FOR SEQ ID NO:67

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 790 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

30

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

35

Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser

	1		5		10		15									
	Tyr	Ile	Val	Arg	Ile	Ala	Ala	Ile	Leu	Cys	Leu	Phe	Val	Gly	Arg	Pro
			20				25						30			
	Leu	Phe	Ala	Gln	Ser	Tyr	Val	Asp	Tyr	Val	Asp	Pro	Leu	Ile	Gly	Thr
5			35				40						45			
	Leu	Ser	Ser	Phe	Glu	Leu	Ser	Ala	Gly	Asn	Thr	Tyr	Pro	Val	Ile	Gly
		50					55					60				
	Leu	Pro	Trp	Gly	Met	Asn	Ser	Trp	Thr	Pro	Met	Thr	Gly	Val	Pro	Gly
	65					70					75				80	
10	Asp	Gly	Trp	Gln	Tyr	Thr	Tyr	Ser	Ala	His	Lys	Ile	Arg	Gly	Phe	Lys
				85						90				95		
	Gln	Thr	His	Gln	Pro	Ser	Pro	Trp	Ile	Asn	Asp	Tyr	Gly	Gln	Phe	Ser
			100						105				110			
	Leu	Leu	Pro	Leu	Thr	Ala	Pro	Gln	Lys	Pro	Ser	Ser	Asn	Asp	Ser	Ile
15			115					120					125			
	Ala	Leu	Thr	Lys	Trp	Cys	Lys	Gln	Leu	Phe	Ser	Asp	Glu	Gln	Thr	Ser
		130					135					140				
	Trp	Phe	Ser	His	Lys	Ala	Glu	Thr	Ala	Thr	Pro	Tyr	Tyr	Tyr	Ser	Val
	145				150					155					160	
20	Tyr	Leu	Ala	Asp	Tyr	Asp	Thr	Arg	Val	Glu	Met	Ala	Pro	Thr	Glu	Arg
				165						170				175		
	Ala	Ala	Ile	Phe	Arg	Ile	Arg	Tyr	Ser	Gly	Asn	Thr	Glu	Ser	Gly	Ser
			180					185					190			
	Gly	Arg	Trp	Leu	Arg	Leu	Asp	Ala	Phe	Thr	Gly	Gly	Ser	Glu	Ile	Ser
25			195					200					205			
	Ile	Val	Asp	Pro	His	Thr	Val	Val	Gly	Ile	Ser	Arg	Lys	Asn	Ser	Gly
		210					215					220				
	Gly	Val	Pro	Ala	Asn	Phe	Ala	Cys	Tyr	Phe	Ile	Leu	Gln	Ser	Asp	Thr
	225				230				235					240		
30	Pro	Met	Ala	Asp	Val	Leu	Leu	Glu	Thr	Asp	Thr	Gly	Lys	Ser	Asp	Glu
				245					250				255			
	Gly	Thr	Arg	Ala	Trp	Ala	Ala	Cys	Arg	Phe	Asp	Ser	Gln	Glu	Val	Thr
			260					265					270			
	Val	Arg	Val	Ala	Ser	Ser	Phe	Ile	Ser	Val	Glu	Gln	Ala	Glu	Arg	Asn
35			275					280					285			
	Leu	Ala	Glu	Val	Lys	Gly	Gln	Ser	Phe	Asp	Arg	Ile	Arg	Leu	Ala	Gly

	290	295	300
	Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly		
	305	310	315 320
	Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu		
5	325	330	335
	Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val		
	340	345	350
	His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr		
	355	360	365
10	Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn		
	370	375	380
	Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn		
	385	390	395 400
	Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His		
15	405	410	415
	Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala		
	420	425	430
	Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly		
	435	440	445
20	Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly		
	450	455	460
	Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp		
	465	470	475 480
	Ala Gly Ile Asp Glu Ser Ala Ala Arg Thr Leu Glu Tyr Ala Tyr Asn		
25	485	490	495
	Asp Trp Cys Ile Leu Arg Leu Gly Arg Thr Leu Gly Trp Asp Arg Ala		
	500	505	510
	Ala Leu Asp Thr Leu Ala His Arg Ser Met Asn Tyr Arg His Leu Phe		
	515	520	525
30	Asp Pro Glu Thr Lys Leu Met Arg Gly Arg Asn Gln Asp Gly Ser Phe		
	530	535	540
	Arg Thr Pro Phe Ser Pro Phe Lys Trp Gly Asp Val Phe Thr Glu Gly		
	545	550	555 560
	Asn Ala Trp His Tyr Thr Trp Ser Val Phe His Asp Val Gln Gly Leu		
35	565	570	575
	Ile Asp Leu Met Gly Gly Asp Arg Pro Phe Val Ser Met Leu Asp Ser		

	580		585		590
	Val Phe Asn Thr Pro Pro Met Phe Asp Glu Ser Tyr Tyr Gly Phe Val				
	595		600		605
	Ile His Glu Ile Arg Glu Met Gln Ile Ala Asp Met Gly Asn Tyr Ala				
5	610		615		620
	His Gly Asn Gln Pro Ile Gln His Met Ile Tyr Leu Tyr Asn His Ala				
	625		630		635 640
	Gly His Pro Trp Lys Ala Gln Glu Arg Leu Arg Glu Val Met Gly Arg				
		645		650	655
10	Leu Tyr Arg Pro Thr Pro Asp Gly Tyr Cys Gly Asp Glu Asp Asn Gly				
		660		665	670
	Gln Thr Ser Ala Trp Tyr Val Phe Ser Ala Leu Gly Phe Tyr Pro Val				
		675		680	685
	Thr Pro Ala Thr Asp Gln Tyr Val Leu Gly Ser Pro Ile Phe Ser Lys				
15	690		695		700
	Val Ile Leu Ser Phe Pro Asp Gly His Lys Thr Val Leu His Ala Pro				
	705		710		715 720
	Ala Asn Ser Ala Asp Thr Pro Tyr Ile Arg Ser Ile Ser Val Glu Gly				
		725		730	735
20	Lys Glu Trp Ser Cys Asn Tyr Leu Thr His Glu Gln Leu Arg Ser Ser				
		740		745	750
	Ala Ser Ile Gln Trp Met Met Asp Thr Lys Pro Asn Tyr Asn Arg Gly				
		755		760	765
	Met Lys Glu Ser Asp Arg Pro Tyr Ser Phe Ser Thr Glu Gln Gln Arg				
25	770		775		780
	Arg Ala Asn His Ser Asn				
	785		790		

(2) INFORMATION FOR SEQ ID NO:68

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...452

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

```

Leu Ile Ile Glu Lys Glu Met Lys Thr Thr Val Gln Gln Ile Ile Leu
1           5           10           15
15 Cys Leu Ala Leu Met Met Ser Gly Val Leu Gly Gly Asn Ala Gln Ser
      20           25           30
Phe Trp Glu Glu Ile Ala Pro Pro Phe Ile Ser Asn Glu Pro Asn Val
      35           40           45
Lys Tyr Ile Ile Pro Asn Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr
20      50           55           60
Val Thr Val Thr Lys Arg Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu
65           70           75           80
Gln Leu Gly Met Tyr Tyr Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp
      85           90           95
25 Lys His Asp Pro Tyr Phe Asp Asp Lys Ile Val Ala Asp Ile Gln Thr
      100           105           110
Asp Ala Tyr Gly Arg Val Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln
      115           120           125
Glu Tyr Gln Leu Tyr Ile Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe
30      130           135           140
Lys Thr Ser Val Ser Thr Tyr Glu His Gly Met Ala Val Phe Arg Ser
145           150           155           160
Ser Thr Gly Val Thr Tyr Ile Gly Thr Arg His His Ile Phe Ala Ser
      165           170           175
35 Gly Val Asn Asp Phe Glu Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro
      180           185           190

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Met Ser Cys Arg Phe Ala Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu
 195 200 205
 Ala Leu Met His Glu Thr Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln
 210 215 220
 5 Asn Gly Glu Phe Val Asp Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile
 225 230 235 240
 Ile Ala Ser Met Cys Ser Asn Lys Glu Gly Asp Ile Ile Ala Leu Val
 245 250 255
 Thr Ser Tyr Thr Gly Phe Met Ser Gly Thr Leu Ala Ile Arg Lys Ala
 10 260 265 270
 Asp Glu Gly Lys Trp Gln Leu Val Gly Gly Asp Ile Gln Asn Ala Ile
 275 280 285
 Val Gln Asn Ile Cys Met Met Asp Asp Asn Lys Ile Ala Cys Glu Val
 290 295 300
 15 Phe Gly Thr Pro Asn Gly Val Asp Gly Arg Thr Arg Val Cys Val Ser
 305 310 315 320
 Asp Ala Ser Val Phe Asp Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly
 325 330 335
 Gly Leu Ile Phe Asp Thr Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu
 20 340 345 350
 Tyr Ala Lys Phe Gly Gly Ile Met Leu Arg Ser Lys Glu Ser Phe Ile
 355 360 365
 Thr Ser Phe Ile Ser Pro Thr Val Val Gln Gly Val Asp Val Tyr Thr
 370 375 380
 25 Leu Ala Gly Lys Ile Arg Ile Glu Ser Glu Thr Pro Val Ser Glu Val
 385 390 395 400
 Leu Leu Phe Asp Leu Ala Gly Arg Met Val Leu Arg Gln Thr Ile Asp
 405 410 415
 Asn Lys Ile Tyr Ser Asp Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly
 30 420 425 430
 Ile Tyr Val Val Ser Val Arg Leu Ser Ser Gly Gln Val Phe Ser His
 435 440 445
 Lys Val Gln Val
 450
 35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

15 (A) NAME/KEY: misc_feature

(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

20 Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly
 1 5 10 15
 Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg
 20 25 30
 Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser
 25 35 40 45
 Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val
 50 55 60
 Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His
 65 70 75 80
 30 Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe
 85 90 95
 Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His
 100 105 110
 Arg Ser Ser Leu Gln Leu Asn Glu Glu Leu Asn Phe Ala Ala Glu Arg
 35 115 120 125
 Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val

	130		135		140	
	Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn					
	145		150		155	160
	Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly					
5		165		170		175
	Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His					
		180		185		190
	Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala					
		195		200		205
10	Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr					
		210		215		220
	Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg					
	225		230		235	240
	Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val					
15		245		250		255
	Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser					
		260		265		270
	Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly					
		275		280		285
20	Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly					
		290		295		300
	Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr					
	305		310		315	320
	Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys					
25		325		330		

(2) INFORMATION FOR SEQ ID NO:70

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

10

```

Ile Lys Arg Ile Glu Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu
1           5           10           15
Leu Ala Ser Val Thr Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg
           20           25           30
15 Val Asp Ala Asn Phe Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly
           35           40           45
Tyr Val Trp Asp Thr Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala
           50           55           60
Ala Glu Phe Met Ile Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu
20 65           70           75           80
Asn Tyr Thr Met Lys Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met
           85           90           95
Val Pro Gly Thr Tyr Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu
           100          105          110
25 Gln Leu Pro Ile Asn Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met
           115          120          125
Ala Val Ser Ile Glu Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly
           130          135          140
Thr Tyr Arg Gln Lys Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr
30 145          150          155          160
Glu Phe Phe Gly Pro Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp
           165          170          175
Ile Gly Ala Asn Ile Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile
           180          185          190
35 Gln Ile Gly Tyr Glu His Gly Phe Val Asp Ile Val Ser Gly Gly Gly
           195          200          205

```

Ser Asp Ile Pro Arg Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr
 210 215 220
 Ala Leu Arg Glu Lys Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe
 225 230 235 240
 5 Phe Val Gly Ile Gly Tyr Arg Phe
 245

(2) INFORMATION FOR SEQ ID NO:71

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...563

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

Ser Leu Ile Asn Asn Ser Arg Asp Trp Arg Ala Pro Val Arg Leu Ser
 1 5 10 15
 30 Leu Lys Lys Lys Thr Lys Thr Met Lys Thr Lys Val Leu Arg Lys Phe
 20 25 30
 Val Val Ala Ala Phe Ala Val Ala Thr Leu Cys Pro Leu Ala Gln Ala
 35 40 45
 Gln Thr Met Gly Gly Asp Asp Val Lys Val Val Gln Tyr Asn Gln Glu
 35 50 55 60
 Lys Leu Val Gln Thr Arg Met Ser Val Ala Asp Asn Gly Trp Ile Tyr

	65		70		75		80									
	Val	Met	Thr	His	Ser	Gly	Tyr	Asp	Thr	Gly	Asn	Ser	Asn	Val	Lys	Ile
				85					90						95	
	Phe	Arg	Ser	Lys	Asp	Gln	Gly	Ala	Thr	Tyr	Gln	Lys	Leu	Arg	Asp	Trp
5				100				105						110		
	Asp	Pro	Ser	Asp	Asp	Tyr	Gln	Phe	Gln	Asp	Phe	Asp	Ile	Val	Val	Thr
				115				120					125			
	Gly	Lys	Asn	Glu	Ser	Asp	Ile	Lys	Ile	Trp	Ser	Val	Glu	Leu	Met	Asn
				130				135					140			
10	Lys	Pro	Gly	Gly	Tyr	Lys	Ser	Arg	Val	Ala	Val	Phe	Ser	Arg	Asp	Ala
	145					150				155					160	
	Asn	Ala	Gln	Asn	Ala	Lys	Leu	Val	Tyr	Lys	Glu	Asp	Phe	Ser	Asn	Val
				165				170							175	
	Gln	Leu	Tyr	Asp	Val	Asp	Ile	Ala	Ser	Asn	Tyr	Arg	Ser	Pro	Ser	Ser
15				180				185						190		
	Leu	Asn	Asn	Gly	Gly	Asn	Pro	Phe	Ala	Leu	Ala	Phe	Ala	Tyr	Thr	Gly
				195				200					205			
	Phe	Asn	Asn	Thr	His	Lys	Ile	Ser	Phe	Val	Asp	Tyr	Val	Phe	Ser	Leu
	210					215						220				
20	Asn	Gly	Gly	Gln	Asn	Phe	Asn	Lys	Asn	Leu	Leu	Phe	Ser	Gln	Asp	Gly
	225					230				235					240	
	Glu	Lys	Lys	Ile	Asp	Lys	Val	Asp	Leu	Ser	Leu	Gly	Ser	Thr	Ser	Glu
				245				250					255			
	Ser	Met	Gly	His	Asn	Ala	Trp	Pro	Leu	Met	Gly	Val	Val	Phe	Glu	Met
25				260				265					270			
	Asn	Lys	Gln	Gly	Gly	Lys	Ser	Asp	Ile	Gly	Phe	Leu	Ser	Asn	Phe	Val
				275				280					285			
	Asp	Asn	Asp	Pro	Glu	Phe	Gln	Trp	Ser	Gly	Pro	Ile	Lys	Val	Ser	Glu
	290					295						300				
30	Ser	Asp	Met	Ser	Phe	Ser	Pro	Lys	Ile	Gln	Met	Leu	Leu	Asp	Glu	Asp
	305					310				315					320	
	Asn	Asn	Thr	Ile	Asn	Gly	Glu	Ser	Cys	His	Asn	Phe	Met	Ile	Thr	Tyr
				325				330					335			
	Ser	Asp	Tyr	Asp	Ser	Glu	Tyr	Ser	Asp	Trp	Asp	Ile	Arg	Tyr	Val	Tyr
35				340				345					350			
	Pro	Lys	Lys	Ser	Phe	Lys	Tyr	Glu	Lys	Gly	Lys	Thr	Pro	Thr	Met	Asp

	355		360		365											
	Asp	Leu	Val	Glu	Ala	Phe	Leu	Thr	Ala	Ser	Tyr	Gln	Ser	Glu	Thr	Asn
	370						375						380			
	Ser	Gly	Leu	Gly	Tyr	Asp	Lys	Asn	Ala	Asn	His	Tyr	Leu	Ile	Thr	Tyr
5	385					390					395				400	
	Ala	Lys	Lys	Glu	Glu	Asn	Gly	Thr	Asn	Thr	Leu	Lys	Tyr	Arg	Trp	Ala
				405					410					415		
	Asn	Tyr	Asp	Lys	Ile	His	Asn	Lys	Asp	Leu	Trp	Ser	Asp	Thr	Phe	Thr
			420						425					430		
10	Tyr	Thr	Ser	Ser	Ala	Asn	Ala	Leu	Tyr	Thr	Pro	Gln	Val	Asp	Ile	Asn
		435						440						445		
	Pro	Thr	Lys	Gly	Leu	Val	Cys	Trp	Ser	Trp	Val	Glu	Tyr	Leu	Pro	Gly
		450					455					460				
	Lys	Arg	Ile	Val	Trp	Ser	Asp	Thr	Gln	Trp	Thr	His	Ala	Asn	Gly	Val
15	465				470					475				480		
	Glu	Asp	Ile	Val	Met	Gln	Glu	Gly	Ser	Met	Lys	Leu	Tyr	Pro	Asn	Pro
				485					490					495		
	Ala	Gln	Glu	Tyr	Ala	Val	Ile	Ser	Leu	Pro	Thr	Ala	Ala	Asn	Cys	Lys
		500							505					510		
20	Ala	Val	Val	Tyr	Asp	Met	Gln	Gly	Arg	Val	Val	Ala	Glu	Ala	Ser	Phe
		515						520						525		
	Ser	Gly	Asn	Glu	Tyr	Arg	Leu	Asn	Val	Gln	His	Leu	Ala	Lys	Gly	Thr
		530					535					540				
	Tyr	Ile	Leu	Lys	Val	Val	Ser	Asp	Thr	Glu	Arg	Phe	Val	Glu	Lys	Leu
25	545				550					555				560		
	Ile	Val	Glu													

(2) INFORMATION FOR SEQ ID NO:72

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...378

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

```

Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly
1           5           10           15
15 Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His
           20           25           30
Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala
           35           40           45
Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser
20          50           55           60
Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu
65          70           75           80
Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu
           85           90           95
25 Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp
           100          105          110
Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser
           115          120          125
Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser
30          130          135          140
Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala
145          150          155          160
Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser
           165          170          175
35 Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe
           180          185          190

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Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser
 195 200 205
 Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu
 210 215 220
 5 Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala
 225 230 235 240
 Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu
 245 250 255
 Gly Ala Tyr Trp Gly Trp Thr Asn Asp Ala His Ile Leu Phe Ser Pro
 10 260 265 270
 Ile Pro Lys Ser Lys Val His Tyr Asp Thr Tyr Thr Arg Ala Gly Ser
 275 280 285
 Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe
 290 295 300
 15 Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile
 305 310 315 320
 Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr
 325 330 335
 Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys
 20 340 345 350
 Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly
 355 360 365
 Phe Asn Phe Thr Val Gly Leu Trp Thr Asn
 370 375

25

(2) INFORMATION FOR SEQ ID NO:73

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

5 (A) NAME/KEY: misc_feature

(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

```

10  Ile Cys Gly Ser Lys Met Asn Leu Ser Gly Leu Gln Ser Phe Thr Met
    1             5             10             15
    Met Lys Ser Met Arg Ser Val Leu Leu Leu Phe Pro Leu Ser Leu
        20             25             30
    Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
15      35             40             45
    Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
        50             55             60
    Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
    65             70             75             80
20  Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
        85             90             95
    Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
        100            105            110
    Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
25      115            120            125
    Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
        130            135            140
    Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
    145            150            155            160
30  Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
        165            170            175
    Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
        180            185            190
    Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
35      195            200            205
    Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile

```

210 215 220
 Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
 225 230 235 240
 Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
 5 245 250 255
 Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
 260 265 270
 Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
 275 280 285

10

(2) INFORMATION FOR SEQ ID NO:74

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids
 15 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

30

Gly Glu Tyr Pro Ala Asn Ser Asn Asp Lys Lys Glu Met Val Met Lys
 1 5 10 15
 Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu Ile Thr
 20 25 30
 35 Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp Ile Tyr
 35 40 45

	Thr	Ser	Arg	Lys	Glu	Ile	Arg	Lys	Gln	Asn	Gln	Val	Lys	Asp	Trp	Gln	
	50						55						60				
	Asn	Gln	Glu	Asp	Gly	Tyr	Gly	Asp	Asp	Thr	Glu	Tyr	Thr	Val	Ala	Ser	
	65						70				75					80	
5	Asp	Arg	Asp	Ile	Asp	Ala	Tyr	Asn	Arg	Arg	Asp	Gly	Gln	Ser	Tyr	Asp	
							85				90					95	
	Gly	Lys	Lys	Leu	Ser	Lys	Asp	Lys	Lys	Arg	Asp	Ser	Thr	Arg	Ser	Ser	
							100				105					110	
	Val	Pro	Gly	Arg	Tyr	Ser	Arg	Arg	Leu	Ala	Arg	Phe	Tyr	Lys	Pro	Asn	
10							115				120					125	
	Thr	Ile	Val	Ile	Ser	Gly	Ala	Asp	Asn	Val	Tyr	Val	Thr	Asp	Asp	Gly	
	130						135								140		
	Glu	Tyr	Phe	Val	Tyr	Gly	Asp	Glu	Tyr	Tyr	Asp	Asp	Ala	Ser	Ser	Val	
	145						150				155					160	
15	Asn	Ile	Tyr	Ile	Asn	Ser	Pro	Trp	Cys	Asp	Pro	Phe	Pro	Tyr	Thr	Ser	
							165				170					175	
	Trp	Tyr	Pro	Ser	Phe	Ser	Gly	Trp	Tyr	Asn	Tyr	Thr	Trp	Asn	Tyr	Pro	
							180				185					190	
	Trp	Phe	Tyr	Tyr	Gly	Ser	His	Ile	Gly	Trp	Gly	Gly	Tyr	Tyr	Pro	Gly	
20							195				200					205	
	Tyr	Asn	Trp	Tyr	Trp	Ser	Tyr	Tyr	Tyr	Asp	Pro	Phe	Tyr	Asn	Pro	Tyr	
	210						215								220		
	Gly	Ile	Gly	Met	Gly	Trp	Gly	Tyr	Pro	Tyr	Gly	Trp	Gly	Ser	Tyr	Tyr	
	225						230				235					240	
25	Gly	Trp	Gly	Gly	Tyr	Pro	Gly	Val	Ile	His	His	Tyr	His	His	Tyr	Pro	
							245				250					255	
	Lys	Lys	Thr	Tyr	Ser	Asn	Gly	Gln	His	Ser	Gly	Ala	Tyr	Tyr	Ser	Tyr	
							260				265					270	
	Gly	Arg	Pro	Asn	Arg	Ile	Lys	Gly	Gly	Thr	Ser	Gly	Ala	Lys	Leu	Gly	
30							275				280					285	
	Thr	Gly	Arg	Tyr	Asp	Arg	Ile	Gln	Asn	Ser	Ser	Ser	Gln	Lys	Asn	Lys	
	290						295								300		
	Phe	Gly	Leu	Gln	Ser	Asn	Lys	Pro	Asn	Asn	Asn	Leu	Gln	Asn	Val	Lys	
	305						310				315					320	
35	Ser	Gly	Arg	Thr	Gly	Arg	Ala	Asn	Arg	Asp	Arg	Asn	Ile	Glu	Thr	Val	
							325				330					335	

Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln Gln Asn
 340 345 350
 Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser Glu Arg
 355 360 365
 5 Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg Ser Asn
 370 375 380
 Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly Ser Met
 385 390 395 400
 Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 10 405 410

(2) INFORMATION FOR SEQ ID NO:75

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 20

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*
 25

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...211

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Leu Val Val Leu Leu
 1 5 10 15
 Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
 35 20 25 30
 Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly

	35		40		45
	Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu				
	50		55		60
	Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn				
5	65		70		75
	Ala Asp Ser Phe Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn				
		85		90	95
	Met Ser Ser Pro Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala				
		100		105	110
10	Asn Cys Tyr Met Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp				
		115		120	125
	Gln Asn Ser Arg His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser				
		130		135	140
	Asn Lys His Asn Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val				
15	145		150		155
	Ser Ile Tyr Thr Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val				
		165		170	175
	Ala Tyr Glu Tyr Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val				
		180		185	190
20	Met Tyr Asp His Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser				
		195		200	205
	Thr His Phe				
	210				

25 (2) INFORMATION FOR SEQ ID NO:76

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

5 (B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

```

10  1   Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met
      5           10           15
      Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala
          20           25           30
      Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr
          35           40           45
15  50  Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn
      55           60
      Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn
      65           70           75           80
      Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp
20      85           90           95
      Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His
          100           105           110
      Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu
          115           120           125
25  130 Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly Ser
      135           140
      Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu
      145           150           155           160
      Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala
30      165           170           175
      Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn
          180           185           190
      Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu
          195           200           205
35  210 Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr
      215           220

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	Asn	Pro	Gln	Ala	Val	Phe	Arg	Gln	Tyr	Phe	Val	Leu	Gln	Val	Ser	Arg	
	225					230				235						240	
	Arg	Pro	Ile	Ser	Ala	Gly	Tyr	Trp	Lys	Lys	Gln	Pro	Pro	Met	Thr	Val	
						245				250						255	
5	Glu	Ala	Gln	Trp	Asp	Ser	Thr	Ala	Gly	Lys	Tyr	Lys	Gln	Tyr	Asp	Gly	
						260				265						270	
	Tyr	Lys	Arg	Glu	Met	Ser	Gly	Asp	Asp	Ile	Gly	Val	Arg	Phe	Ser	Phe	
						275				280						285	
	Asn	Cys	Asp	Gln	Gly	Glu	Lys	Ile	Tyr	Val	Arg	Ser	Ala	Val	Ser	Phe	
10		290					295				300						
	Val	Ser	Glu	Ala	Asn	Ala	Leu	Tyr	Asn	Leu	Glu	Ala	Glu	Gln	Glu	Glu	
	305					310				315						320	
	Val	Phe	Lys	Ser	Val	Gly	Gly	Asn	Pro	Ala	Lys	Ala	Phe	Ser	Ala	Ile	
						325				330						335	
15	Arg	Ser	Arg	Ala	Ile	Glu	Arg	Trp	Glu	Glu	Ala	Leu	Gly	Thr	Val	Glu	
						340				345						350	
	Val	Glu	Gly	Gly	Thr	Pro	Asp	Glu	Lys	Thr	Ile	Phe	Tyr	Thr	Ala	Leu	
						355				360						365	
	Tyr	His	Leu	Leu	Ile	His	Pro	Asn	Ile	Leu	Gln	Asp	Ala	Asn	Gly	Glu	
20		370					375				380						
	Tyr	Pro	Met	Met	Gly	Ser	Gly	Lys	Thr	Gly	Asn	Thr	Ala	His	Asp	Arg	
	385					390				395						400	
	Tyr	Thr	Val	Phe	Ser	Leu	Trp	Asp	Thr	Tyr	Arg	Asn	Val	His	Pro	Leu	
						405				410						415	
25	Leu	Cys	Leu	Leu	Tyr	Pro	Glu	Lys	Gln	Leu	Asp	Met	Val	Arg	Thr	Leu	
						420				425						430	
	Ile	Asp	Met	Tyr	Arg	Glu	Ser	Gly	Trp	Leu	Pro	Arg	Trp	Glu	Leu	Tyr	
						435				440						445	
	Gly	Gln	Glu	Thr	Leu	Thr	Met	Glu	Gly	Asp	Pro	Ser	Leu	Ile	Val	Ile	
30		450					455				460						
	Asn	Asp	Thr	Trp	Gln	Arg	Gly	Leu	Arg	Ala	Phe	Asp	Thr	Ala	Thr	Ala	
	465					470				475						480	
	Tyr	Glu	Ala	Met	Lys	Lys	Asn	Ala	Ser	Ser	Ala	Gly	Ala	Thr	His	Pro	
						485				490						495	
35	Ile	Arg	Pro	Asp	Asn	Asp	Asp	Tyr	Leu	Thr	Leu	Gly	Phe	Val	Pro	Leu	
						500				505						510	

	Arg	Glu	Gln	Tyr	Asp	Asn	Ser	Val	Ser	His	Ala	Leu	Glu	Tyr	Tyr	Leu	
	515				520				525								
	Ala	Asp	Trp	Asn	Leu	Ser	Arg	Phe	Ala	His	Ala	Leu	Gly	His	Lys	Glu	
	530				535				540								
5	Asp	Ala	Ala	Leu	Phe	Gly	Lys	Arg	Ser	Leu	Gly	Tyr	Arg	His	Tyr	Tyr	
	545				550				555				560				
	Asn	Lys	Glu	Tyr	Gly	Met	Leu	Cys	Pro	Leu	Leu	Pro	Asp	Gly	Ser	Phe	
	565				570				575								
	Leu	Thr	Pro	Phe	Asp	Pro	Lys	Gln	Gly	Glu	Asn	Phe	Glu	Pro	Asn	Pro	
10	580				585				590								
	Gly	Phe	His	Glu	Gly	Ser	Ala	Tyr	Asn	Tyr	Ala	Phe	Phe	Val	Pro	His	
	595				600				605								
	Asp	Ile	Gln	Gly	Leu	Ala	Arg	Leu	Met	Gly	Gly	Ala	Lys	Val	Phe	Ser	
	610				615				620								
15	Glu	Arg	Leu	Gln	Lys	Val	Phe	Asp	Glu	Gly	Tyr	Tyr	Asp	Pro	Thr	Asn	
	625				630				635				640				
	Glu	Pro	Asp	Ile	Ala	Tyr	Pro	Tyr	Leu	Phe	Ser	Tyr	Phe	Pro	Lys	Glu	
	645				650				655								
	Ala	Trp	Arg	Thr	Gln	Lys	Leu	Thr	Arg	Glu	Leu	Ile	Asp	Lys	His	Phe	
20	660				665				670								
	Cys	Asn	Ala	Pro	Asn	Gly	Leu	Pro	Gly	Asn	Asp	Asp	Ala	Gly	Thr	Met	
	675				680				685								
	Ser	Ala	Trp	Leu	Val	Tyr	Ser	Met	Leu	Gly	Phe	Tyr	Pro	Asp	Cys	Pro	
	690				695				700								
25	Gly	Ser	Pro	Thr	Tyr	Thr	Leu	Thr	Ser	Pro	Val	Phe	Pro	Arg	Val	Arg	
	705				710				715				720				
	Ile	Arg	Leu	Asn	Pro	Gln	Tyr	Tyr	Pro	Gln	Gly	Glu	Leu	Ile	Ile	Thr	
	725				730				735								
	Thr	Asn	Thr	Glu	Asn	Gln	Pro	Thr	Asp	Ser	Ile	Tyr	Ile	His	Thr	Val	
30	740				745				750								
	Ser	Leu	Gly	Asn	Lys	Thr	Leu	Pro	His	Gly	Thr	Arg	His	Ile	Ser	His	
	755				760				765								
	Ala	Asp	Leu	Val	Arg	Cys	Gly	His	Leu	Arg	Tyr	Glu	Leu	Ser	Asn	Arg	
	770				775				780								
35	Pro	Arg															
	785																

(2) INFORMATION FOR SEQ ID NO:77

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 953 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...953

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

Ile Arg Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu
 1 5 10 15
 Pro Val Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu
 25 20 25 30
 Arg Pro Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala
 35 40 45
 Leu Ser Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile
 50 55 60
 30 Pro Asp Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser
 65 70 75 80
 Met Arg Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile
 85 90 95
 Val Glu Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg
 35 100 105 110
 Ala Tyr Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu

	115		120		125
	Glu Ala Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr				
	130		135		140
	Arg Tyr Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe				
5	145		150		155
	Lys Asp Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe				
		165		170	175
	Arg Thr Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu				
		180		185	190
10	Gly Tyr Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met				
		195		200	205
	Phe Met Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro				
		210		215	220
	His Phe Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp				
15	225		230		235
	Ile Val Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro				
		245		250	255
	Ile Gly Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser				
		260		265	270
20	Gly Ile Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr				
		275		280	285
	Leu Arg Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu				
		290		295	300
	Ala Leu Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala				
25	305		310		315
	Gln Ser Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala				
		325		330	335
	Asn Tyr Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr				
		340		345	350
30	Ser Lys Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro				
		355		360	365
	Lys Ala Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr				
		370		375	380
	Gly Ser Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala				
35	385		390		395
	Arg Thr Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe				

		405		410		415													
		Pro	Gly	Thr	Pro	Phe	Ser	Ile	Thr	Gly	Ser	Met	Asp	Ile	Ser	Gln	Asn		
		420								425					430				
		Met	Arg	Asp	Thr	Thr	Val	Ser	Leu	Thr	Leu	Pro	Asn	Leu	Ser	Ile	Asn		
5		435							440					445					
		Met	Ser	Thr	Arg	Tyr	Pro	Phe	Lys	Arg	Lys	Thr	Arg	Val	Gly	Pro	Glu		
		450						455					460						
		Arg	Trp	Tyr	Glu	Lys	Leu	Ser	Val	Gly	Tyr	Ser	Gly	Gln	Leu	Arg	Asn		
		465				470					475				480				
10		Ser	Ile	Leu	Thr	Lys	Glu	Lys	Asp	Leu	Leu	Gln	Ser	Asn	Leu	Val	Arg		
						485					490				495				
		Asp	Trp	Lys	Asn	Gly	Met	Arg	His	Ser	Val	Pro	Ile	Ser	Leu	Thr	Val		
					500					505				510					
		Pro	Leu	Leu	Asp	Tyr	Ile	Asn	Leu	Thr	Met	Gly	Val	Asn	Tyr	Asn	Glu		
15		515						520					525						
		Trp	Trp	Tyr	Thr	Lys	Gly	Ile	Arg	Lys	Ser	Trp	Asn	Glu	Asp	Lys	Lys		
		530					535					540							
		Thr	Phe	Leu	Pro	Ser	Asp	Thr	Thr	Tyr	Lys	Phe	Arg	Arg	Leu	Tyr	Asp		
		545				550					555			560					
20		Tyr	Ser	Leu	Ser	Ala	Gly	Leu	Ser	Thr	Thr	Leu	Tyr	Gly	Met	Phe	Lys		
						565					570			575					
		Pro	Trp	Lys	Pro	Phe	Ser	Phe	Gly	Gly	Asn	Leu	Ile	Met	Ile	Arg	His		
					580					585				590					
		Arg	Phe	Thr	Pro	Thr	Val	Ser	Phe	Ser	Tyr	Met	Pro	Asp	Phe	Thr	Lys		
25		595						600					605						
		Arg	Arg	Tyr	Gly	Phe	Trp	Glu	Leu	Leu	Glu	His	Thr	Asp	Gln	Asn	Gly		
		610					615					620							
		Lys	Leu	His	Thr	Leu	Leu	Tyr	Ser	Pro	Tyr	Phe	Glu	Gln	Ile	Phe	Gly		
		625				630					635			640					
30		Ala	Pro	Ser	Met	Gly	Asn	Ala	Gly	Ser	Val	Asn	Phe	Ser	Phe	Asp	Asn		
						645					650			655					
		Asn	Leu	Glu	Ala	Lys	Ile	Lys	Ser	Lys	Ser	Asp	Ser	Thr	Gly	Ile	Lys		
					660					665				670					
		Lys	Ile	Ser	Leu	Ile	Asp	Gln	Phe	Thr	Trp	Ser	Thr	Ser	Tyr	Asn	Met		
35		675						680					685						
		Phe	Ala	Asp	Ser	Ile	Arg	Trp	Ser	Asn	Ile	Ser	Ala	Ser	Leu	Ala	Leu		

	690		695		700											
	Arg	Leu	Ser	Lys	Ser	Phe	Thr	Leu	Arg	Leu	Ser	Gly	Leu	Phe	Asp	Pro
	705					710						715				720
	Tyr	Leu	Thr	Lys	Tyr	Tyr	Glu	Gly	Glu	Asp	Gly	Lys	Ile	Ile	Pro	Tyr
5					725						730				735	
	Lys	Ser	Asn	Asp	Leu	Arg	Ile	Phe	Asn	Gly	Lys	Gly	Leu	Ala	Arg	Leu
				740						745				750		
	Ile	Ser	Thr	Gly	Thr	Ser	Phe	Ser	Tyr	Thr	Leu	Asn	Lys	Glu	Ser	Leu
			755					760					765			
10	Ser	Gly	Leu	Ile	Ala	Leu	Phe	Ser	Gly	Lys	Lys	Glu	Arg	Arg	Asp	Glu
	770						775					780				
	Lys	Lys	Asn	Thr	Gly	Ala	Thr	Pro	His	Glu	Gly	Asp	Asp	Ala	Ala	Asp
	785				790					795						800
	Ile	Leu	Glu	Gly	Gly	Arg	Pro	Gln	Asn	Glu	Ser	Gly	Gly	Ser	Leu	Leu
15				805						810					815	
	Glu	Arg	Asn	Arg	Gln	Gly	Gly	Ala	Val	Asp	Gln	Asp	Gly	Tyr	Phe	Ala
			820					825					830			
	Tyr	Ser	Ile	Pro	Trp	Ser	Leu	Ser	Phe	Asp	Tyr	Ser	Trp	Asn	Ile	Ala
		835					840						845			
20	Thr	Asp	Tyr	Asn	Arg	Tyr	Asn	Val	Asn	Lys	Met	Glu	His	Tyr	Tyr	Arg
	850					855						860				
	Val	Thr	Gln	Asn	Leu	Ser	Phe	Arg	Gly	Asn	Ile	Gln	Pro	Thr	Pro	Asn
	865				870					875						880
	Trp	Ser	Phe	Gly	Phe	Asn	Ala	Asn	Tyr	Asn	Phe	Asp	Leu	Lys	Lys	Ile
25				885						890					895	
	Thr	Ser	Leu	Thr	Cys	Asn	Val	Thr	Arg	Asp	Met	His	Cys	Trp	Ala	Ile
			900					905					910			
	Ser	Ala	Ser	Phe	Ile	Pro	Ile	Gly	Ala	Tyr	Lys	Ser	Tyr	Asn	Phe	Val
		915						920					925			
30	Ile	Ser	Val	Lys	Ser	Ser	Leu	Leu	Gln	Asp	Leu	Lys	Tyr	Gln	Gln	Ser
	930						935						940			
	Asn	Arg	Pro	Ile	Thr	Asn	Thr	Trp	Tyr							
	945					950										

35 (2) INFORMATION FOR SEQ ID NO:78

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15

(B) LOCATION 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

	Ser	Asn	Ser	Ser	Ser	His	Lys	Trp	Leu	Ile	Tyr	Tyr	His	Ile	Glu	Lys
20	1				5					10					15	
	Thr	Lys	Ser	Ile	Met	Ile	Arg	Lys	Leu	Ile	Leu	Leu	Leu	Ala	Leu	Met
				20					25					30		
	Pro	Val	Ala	Ser	Val	Ala	Phe	Ala	Val	Pro	Thr	Asp	Ser	Thr	Glu	Ser
			35				40					45				
25	Lys	Asp	Asn	Arg	Ile	Leu	Thr	Ser	Met	Gln	Ser	Ser	Ser	Leu	Asn	Arg
		50				55				60						
	Asp	Asp	Ala	Pro	Asp	Lys	Trp	Gln	Pro	Met	His	Ala	Asn	Phe	Ser	Ile
	65				70				75					80		
	Gln	Ser	Asp	Met	Leu	Leu	Ser	Thr	Ala	Gln	Lys	Ser	Lys	Asn	Thr	Trp
30				85				90					95			
	Phe	Gly	Asn	Ser	Tyr	Ile	Met	Gly	Ile	Ile	Lys	Asn	Asn	Tyr	Leu	Glu
			100				105					110				
	Phe	Gly	Ala	Arg	Phe	Glu	Asp	Leu	Tyr	Lys	Pro	Leu	Pro	Gly	His	Glu
			115				120					125				
35	Pro	Glu	Met	Unk	Arg	Gly	Val	Pro	His	Met	Tyr	Val	Lys	Gly	Ser	Tyr
		130					135					140				

	His Trp Ala Glu Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser	
	145	150 155 160
	Gly Met Val Phe Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn	
	165	170 175
5	Ala Val Arg Gly Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg	
	180	185 190
	Val Lys Gly Ile Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly	
	195	200 205
	Lys Val Phe Asn Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu	
10	210	215 220
	Leu Asn Val Glu Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His	
	225	230 235 240
	Leu Ala Ile Gly Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp	
	245	250 255
15	Ile Phe Val Gly Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu	
	260	265 270
	Asn Val Pro Ile Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu	
	275	280 285
	Ala Leu Tyr Ala Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp	
20	290	295 300
	Asn Asp Tyr Ile Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser	
	305	310 315 320
	Tyr Ser Lys Lys Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu	
	325	330 335
25	Asn Phe Ala Phe Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met	
	340	345 350
	Ile Asn Tyr Met Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala	
	355	360 365
	Ala Ile Tyr Pro Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln	
30	370	375 380
	Gly Glu Leu Arg Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg	
	385	390 395 400
	Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp	
	405	410 415
35	Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly	
	420	425 430

Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile
 435 440 445
 Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu
 450 455 460
 5 Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala
 465 470 475 480
 Gly Glu Lys Pro Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly
 485 490 495
 Lys Tyr Lys Leu Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr
 10 500 505 510
 Leu His Thr Lys Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu
 515 520 525
 Leu Ser Ile Leu Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn
 530 535 540
 15 Ile Gly Glu Thr Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr
 545 550 555 560
 His Gly Ala His Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly
 565 570 575
 Met Asn Cys Ser Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly
 20 580 585 590
 Phe Tyr Leu Ser Tyr Ser Thr Asn Leu
 595 600

(2) INFORMATION FOR SEQ ID NO:79

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...962

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

```

Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys
1           5           10           15
10 Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln
           20           25           30
Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser
           35           40           45
Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser
15           50           55           60
Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro
65           70           75           80
Asp Phe Asn Pro Glu Asp Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln
           85           90           95
20 Arg Asp Gly Arg Pro Val Arg Ile Gly Gln Val Ile Pro Val Asp Val
           100          105          110
Asp Phe Ala Ser Lys Ala Ser His Ile Ser Ser Ile Gly Asp Val Asp
           115          120          125
Val Tyr Arg Leu Gln Phe Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu
25           130          135          140
Tyr Tyr Asp Ala Phe Asn Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr
145          150          155          160
Thr Pro Asp His Glu Ile Val Leu Gly Ala Tyr Thr Asn Ala Thr His
           165          170          175
30 Arg Arg Asn Gly Ala Phe Ala Thr Glu Pro Val Pro Gly Ser Glu Leu
           180          185          190
Ile Met Asp Tyr Glu Val Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys
           195          200          205
Ile Ser Gly Ala Gly Tyr Ile Phe Asp Lys Val Gly Gly Arg Pro Val
35           210          215          220
Thr Asp Asn His Tyr Gly Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys

```

	225		230		235		240									
	Glu	Ile	Asn	Ile	Asn	Cys	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys
			245					250							255	
	Asn	Gly	Val	Val	Gln	Met	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met
5			260					265							270	
	Cys	Ser	Gly	Asn	Leu	Leu	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu
			275					280						285		
	Ile	Ile	Ser	Ala	Gly	His	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val
			290					295					300			
10	Thr	Gln	Ser	Glu	Leu	Asp	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys
	305						310					315				320
	Arg	Gly	Cys	Ser	Asn	Gly	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile
							325				330				335	
	Ile	Gly	Ala	Ser	Met	Lys	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp
15			340					345							350	
	Gly	Leu	Leu	Leu	Gln	Leu	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val
			355					360					365			
	Tyr	Tyr	Asn	Gly	Trp	Asp	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala
			370					375					380			
20	Gly	Ile	His	His	Pro	Ala	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys
	385						390				395					400
	Lys	Thr	Pro	Ala	Leu	Asn	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly
							405				410				415	
	Thr	Asp	Asp	His	Phe	Tyr	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly
25			420					425							430	
	Gly	Ser	Ser	Gly	Ser	Ser	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly
			435					440						445		
	Thr	Leu	Thr	Gly	Gly	Ala	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly
			450				455						460			
30	Arg	Leu	Asn	Ser	His	Trp	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser
	465						470					475				480
	Arg	Met	Asp	Ile	Tyr	Leu	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile
							485				490				495	
	Leu	Asn	Gly	Thr	Tyr	Arg	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro
35			500					505						510		
	Arg	Leu	Leu	Leu	Gln	Ser	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr

	515		520		525
	Ala Val Pro Ala Asp Gln Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His				
	530		535		540
	Ile Phe Arg Asn Gly Lys Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr				
5	545		550		555
	Ser Asp Ala Ile Asp Glu Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr				
		565		570	
	Glu Val Ser Ala Arg Phe Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu				
		580		585	
10	Ser Tyr Lys Asp Thr Asp Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp				
		595		600	
	Ile Gln Thr Lys Leu Lys Pro Asp Val Thr Pro Leu Pro Gly Gly Gly				
		610		615	
	Val Ser Leu Ser Trp Lys Val Pro Phe Leu Ser Gln Leu Val Ser Arg				
15	625		630		635
	Phe Gly Glu Ser Pro Asn Pro Val Phe Lys Thr Phe Glu Val Pro Tyr				
		645		650	
	Val Ser Ala Ala Ala Ala Gln Thr Pro Asn Pro Pro Val Gly Val Val				
		660		665	
20	Ile Ala Asp Lys Phe Met Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile				
		675		680	
	Ala Ala Val Tyr Val Met Pro Ser Ala Pro Asp Ser Thr Phe His Leu				
		690		695	
	Phe Leu Lys Ser Asn Thr Asn Arg Arg Leu Gln Lys Val Thr Thr Pro				
25	705		710		715
	Ser Asp Trp Gln Ala Gly Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro				
		725		730	
	Phe Pro Val Asn Asn Asp His Met Leu Phe Ala Gly Ile Arg Met Pro				
		740		745	
30	Asn Lys Tyr Lys Leu Asn Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp				
		755		760	
	Asn Leu Phe Ser Ile Thr Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val				
		770		775	
	Ser Phe Glu Gly Tyr Gly Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile				
35	785		790		795
	Lys Tyr Leu Val Val Asn Thr Asp Ala Pro Lys Ile Asp Met Ser Leu				

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1312

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

```

Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala
1           5           10           15
Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg
10          20          25          30
Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln
          35          40          45
Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser
          50          55          60
15 Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val
65          70          75          80
Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe
          85          90          95
Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu
20          100         105         110
Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu Phe Ser
          115         120         125
Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn
          130         135         140
25 Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu Pro Glu
145         150         155         160
Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr
          165         170         175
Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser Gln Asp
30          180         185         190
Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe
          195         200         205
Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu
          210         215         220
35 Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr
225         230         235         240

```

	Gly	Ile	Phe	Asn	Lys	Val	Ala	Ser	Ser	Ala	Phe	Ile	Asn	Tyr	Glu	Ala	
					245					250					255		
	Asp	Gly	Lys	Ser	Ala	Ile	Glu	Asn	Asp	Met	Val	Phe	Ser	Arg	Gly	Thr	
					260					265					270		
5	Thr	Thr	Tyr	Ile	Ser	Gly	Asn	Val	Ala	Ser	Asn	Leu	Pro	Gln	Asn	Cys	
					275					280					285		
	Asp	Tyr	Leu	Val	Ile	Tyr	Asp	Asp	Met	Phe	Asn	Val	Asn	Gln	Gln	Pro	
					290					295					300		
	His	Asp	Glu	Ile	Lys	Arg	Leu	Cys	Glu	His	Arg	Ala	Phe	Tyr	Asn	Gly	
10	305					310					315					320	
	Phe	Asp	Val	Ala	Ala	Val	Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser	Phe	Pro	
					325					330					335		
	Ser	Asn	Ala	Thr	Ser	Tyr	Ile	Asn	Glu	Thr	Lys	Leu	Lys	Asn	Phe	Ile	
					340					345					350		
15	Arg	Ser	Val	Tyr	Asn	Gln	Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp	Gly	Lys	
					355					360					365		
	Leu	Gly	Tyr	Val	Leu	Leu	Ile	Gly	Lys	Pro	Leu	Ser	Lys	Tyr	Leu	Ala	
					370					375					380		
	Asp	Thr	Asp	Asn	Thr	Lys	Val	Pro	Thr	Ser	Phe	Ile	His	Asn	Val	Ser	
20	385					390					395					400	
	Leu	Ile	Pro	Ser	His	Pro	Thr	Phe	Gly	Ser	Ile	Cys	Ala	Ser	Asp	Tyr	
					405					410					415		
	Phe	Phe	Ser	Cys	Val	Ser	Pro	Leu	Asp	Thr	Val	Gly	Asp	Leu	Phe	Ile	
					420					425					430		
25	Gly	Arg	Phe	Ser	Val	Thr	Asn	Ala	His	Glu	Leu	His	Asn	Leu	Ile	Glu	
					435					440					445		
	Lys	Thr	Ile	Asn	Lys	Glu	Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His	Lys	Asn	
					450					455					460		
	Ile	Leu	Tyr	Ala	Glu	Gly	Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu	Arg	Leu	
30	465					470					475					480	
	Phe	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile	Leu	Lys	
					485					490					495		
	Ser	Asn	Gln	Val	Ser	Ala	Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu	Asn	Asn	
					500					505					510		
35	Gly	Ser	His	His	Phe	Tyr	Phe	Asn	Thr	His	Gly	Met	Pro	Thr	Val	Trp	
					515					520					525		

	Gly	Ile	Gly	Gln	Gly	Leu	Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg	Leu	Asn	
	530						535						540				
	Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser	Ser	Ala	
	545					550					555					560	
5	Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr	Thr	Tyr	
					565					570					575		
	Ala	Pro	Asn	Lys	Gly	Phe	Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg	Ala	Thr	
				580					585					590			
	Gln	Tyr	Ala	Val	Tyr	Leu	Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu	Phe	Tyr	
10			595					600					605				
	Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	Val	Gly	
	610						615					620					
	Glu	Met	Leu	Leu	Ser	Ser	Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp	Thr	Tyr	
	625					630					635					640	
15	Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	Ile	Met	
				645						650					655		
	Ala	His	Gly	Met	Glu	Val	Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn	Asn	Thr	
				660					665					670			
	Ile	Ile	Ser	Ser	Pro	Ile	Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu	Lys	Ile	
20			675					680					685				
	Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	Gln	Val	
	690						695					700					
	Met	Ser	Gly	Gly	Thr	Leu	Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile	Ser	Gly	
	705					710				715						720	
25	Glu	Thr	Gly	Ala	Asn	Pro	Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp	Gly	Leu	
				725						730					735		
	Ala	Ile	Asn	Lys	Gln	Val	Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu	Asn	Leu	
				740					745					750			
	Phe	Ser	Thr	His	Ser	Val	Met	Pro	Lys	Phe	His	Phe	Asp	Ser	Val	Lys	
30			755					760					765				
	Phe	Asn	Ser	Ala	Pro	Leu	Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu	Ile	Ser	
	770					775						780					
	Asn	Cys	Glu	Phe	Thr	Asn	Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn	Cys	Asp	
	785					790					795					800	
35	Leu	Ser	Val	Glu	Asn	Ser	Met	Phe	Ser	Ser	Ser	Gly	Ile	Thr	Val	Phe	
				805						810					815		

	Lys	Pro	Met	Ala	Thr	Ser	Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys	Ala	Lys	
				820					825					830			
	Ile	Thr	Asp	Asn	Thr	Phe	Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr	His	Ile	
			835					840					845				
5	Thr	Asn	Thr	Pro	Gly	Leu	Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile	Lys	Leu	
			850				855					860					
	Asp	Asn	Ile	Pro	Glu	Tyr	Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val	Asn	Cys	
	865					870					875				880		
	Asp	Glu	Ala	Leu	Val	Leu	Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn	Arg	Leu	
10				885						890				895			
	His	Asn	Ile	Thr	Arg	Asn	Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly	Ser	Thr	
				900					905					910			
	Leu	Tyr	Asn	Ser	Tyr	Gly	Ile	Tyr	Asn	Arg	Asn	Lys	Ile	Ser	Asn	Asn	
			915				920						925				
15	His	Ile	Gly	Val	Arg	Leu	Leu	Asn	Asn	Ser	Cys	Phe	Tyr	Phe	Asp	Asn	
			930				935					940					
	Ala	Pro	Val	Ile	Asn	Glu	Glu	Asp	Lys	Gln	Thr	Phe	Ile	Ser	Asn	Arg	
	945					950					955				960		
	Thr	Trp	Gln	Leu	Tyr	Ser	Ser	Asn	Gly	Thr	Phe	Pro	Leu	Asn	Phe	His	
20				965						970				975			
	Tyr	Asn	Ser	Leu	Gln	Gly	Gly	Asp	Thr	Asp	Thr	Trp	Ile	Tyr	Asn	Asp	
				980					985				990				
	Thr	Tyr	Thr	Asn	Arg	Tyr	Ile	Asp	Val	Ser	Asn	Asn	His	Trp	Gly	Asn	
				995				1000					1005+				
25	Asn	Asp	Leu	Phe	Asp	Pro	Asn	Gln	Val	Phe	Asn	Thr	Pro	Asp	Leu	Phe	
			1010				1015					1020					
	Ile	Trp	Ile	Pro	Phe	Trp	Asp	Gly	Leu	Pro	Asn	Gly	Arg	Ser	Gly	Asn	
	1025					1030					1035				1040		
	Ser	Ser	Ala	Glu	Ala	Val	Glu	Phe	Gln	Thr	Ala	Leu	Asp	Cys	Ile	Gly	
30				1045						1050				1055			
	Asn	Ser	Asp	Tyr	Leu	Ser	Ala	Lys	Val	Ala	Leu	Lys	Met	Met	Val	Glu	
				1060				1065					1070				
	Thr	Tyr	Pro	Glu	Ser	Asp	Phe	Ala	Ile	Ala	Ala	Leu	Lys	Glu	Leu	Phe	
				1075				1080					1085				
35	Arg	Ile	Glu	Lys	Met	Ser	Gly	Asn	Asp	Tyr	Glu	Gly	Leu	Lys	Asp	Tyr	
			1090				1095						1100				

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Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr
1105          1110          1115          1120
Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln
          1125          1130          1135
5  Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr
          1140          1145          1150
Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn
          1155          1160          1165
Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu
10  1170          1175          1180
Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val Lys Asn
1185          1190          1195          1200
Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro
          1205          1210          1215
15  Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile
          1220          1225          1230
Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp
          1235          1240          1245
Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser
20  1250          1255          1260
Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser
1265          1270          1275          1280
Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr
          1285          1290          1295
25  Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
          1300          1305          1310

```

(2) INFORMATION FOR SEQ ID NO:81

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30  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 938 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

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35  (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

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(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...938

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

	Ser	Glu	Asn	Tyr	Arg	Tyr	Gly	Lys	Ile	Thr	Asn	Gln	Ile	Met	Ala	Ile	
	1					5				10					15		
	Met	Met	Lys	Ser	Ile	Val	Phe	Arg	Ala	Phe	Leu	Thr	Ile	Leu	Leu	Ser	
15					20				25					30			
	Trp	Ala	Ala	Ile	Thr	Asn	Pro	Thr	Ala	Gln	Glu	Ile	Ser	Gly	Met	Asn	
			35					40					45				
	Ala	Ser	Cys	Leu	Ala	Ala	Pro	Ala	Gln	Pro	Asp	Thr	Ile	Leu	Tyr	Glu	
		50					55					60					
20	Ser	Phe	Glu	Asn	Gly	Pro	Val	Pro	Asn	Gly	Trp	Leu	Glu	Ile	Asp	Ala	
	65					70				75					80		
	Asp	Ala	Asp	Gly	Ala	Thr	Trp	Gly	Ser	Pro	Ser	Gly	Ser	Phe	Ser	Val	
					85				90					95			
	Pro	Tyr	Gly	His	Asn	Gly	Leu	Cys	Thr	Tyr	Ser	His	Ile	Arg	Ser	Gly	
25					100				105					110			
	Ile	Ser	Thr	Ala	Gly	Asn	Tyr	Leu	Ile	Thr	Pro	Asn	Ile	Glu	Gly	Ala	
			115					120					125				
	Lys	Arg	Val	Lys	Tyr	Trp	Val	Cys	Asn	Gln	Tyr	Ser	Thr	Asn	Pro	Glu	
		130					135					140					
30	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	Ile	Glu	Asp	Phe	
	145					150				155					160		
	Val	Leu	Leu	Phe	Asp	Asp	Ser	Ile	Thr	Gly	Lys	Pro	Thr	Pro	Leu	Val	
				165					170				175				
	Trp	Arg	Arg	Arg	Ile	Val	Asp	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	
35					180				185				190				
	Trp	Arg	His	Tyr	Lys	Val	Thr	Asp	Ser	His	Thr	Glu	Phe	Leu	Lys	Leu	

	195	200	205
	Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr		
	210	215	220
	Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp		
5	225	230	235 240
	Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu		
	245	250	255
	Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln		
	260	265	270
10	Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu		
	275	280	285
	Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp		
	290	295	300
	Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr		
15	305	310	315 320
	Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly		
	325	330	335
	Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr		
	340	345	350
20	Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser		
	355	360	365
	Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn		
	370	375	380
	Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp		
25	385	390	395 400
	Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met		
	405	410	415
	Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu		
	420	425	430
30	Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile		
	435	440	445
	Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys		
	450	455	460
	Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr		
35	465	470	475 480
	Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile		

	485	490	495
	Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu		
	500	505	510
	Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn		
5	515	520	525
	Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val		
	530	535	540
	Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu		
	545	550	555
10	Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln		
	565	570	575
	Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu		
	580	585	590
	Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile		
15	595	600	605
	Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met		
	610	615	620
	Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro		
	625	630	635
20	Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu		
	645	650	655
	Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val		
	660	665	670
	Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala		
25	675	680	685
	Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala		
	690	695	700
	Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys		
	705	710	715
30	Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu		
	725	730	735
	Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro		
	740	745	750
	Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu		
35	755	760	765
	Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys		

	770		775		780											
	Lys	Pro	Leu	Gln	Leu	Thr	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu
	785				790				795							800
	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr
5				805					810					815		
	Tyr	Ser	Ser	Arg	Asp	Gly	Gln	Val	Glu	Met	Glu	Tyr	Cys	Val	Thr	Ala
				820					825					830		
	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Asn
				835					840					845		
10	Tyr	Thr	Ile	Thr	Ser	Leu	Asp	Asn	Ile	Gln	Ser	Asp	Thr	Ser	Leu	Lys
				850					855					860		
	Ile	Tyr	Pro	Asn	Pro	Ala	Ser	Tyr	Val	Val	Arg	Ile	Glu	Gly	Leu	Ser
				865					870					875		880
	Arg	Ser	Lys	Ser	Thr	Ile	Glu	Leu	Tyr	Asn	Ala	Leu	Gly	Ile	Cys	Ile
15				885					890					895		
	Leu	Arg	Glu	Glu	Thr	His	Ser	Glu	Lys	Thr	Glu	Ile	Asp	Val	Ser	Arg
				900					905					910		
	Leu	Asn	Asp	Gly	Val	Tyr	Leu	Ile	Lys	Val	Val	Gly	Gly	Asn	Lys	Thr
				915					920					925		
20	Thr	Thr	Glu	Lys	Val	Glu	Ile	Lys	Arg	Pro						
				930					935							

(2) INFORMATION FOR SEQ ID NO:82

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1251 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- 35 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1251

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

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Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro
1           5           10           15
Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile
10           20           25           30
Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile
           35           40           45
Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile
           50           55           60
15 Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn
           65           70           75           80
Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp
           85           90           95
Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro
20           100          105          110
Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro
           115          120          125
Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro
           130          135          140
25 Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr
           145          150          155          160
Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln
           165          170          175
Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile
30           180          185          190
Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala
           195          200          205
Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His
           210          215          220
35 Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile
           225          230          235          240

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	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr	His	Thr	Gln	Gly	Gly	Leu	Lys
					245					250					255	
	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser	Thr	Ala	Val	Asp	Lys	His	Ile
					260				265					270		
5	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr	Glu	Gln	Tyr	Pro	Val	Lys	Asn
					275			280					285			
	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys	Thr	Gly	Asn	Ala	Asn	Asp	Pro
					290			295				300				
	Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile	Asn	Phe	Pro	Thr	Asn	Tyr	Val
10	305					310					315					320
	Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr	Pro	Asn	Tyr	Pro	Thr	His	Ser
					325					330					335	
	Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro	Glu	Ser	Lys	Phe	Asp	Tyr	Ser
					340				345				350			
15	Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp	Gly	Val	Ala	Gly	Ala	Leu	Val
					355			360					365			
	Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr	Tyr	Tyr	Tyr	Phe	Pro	Cys	Asn
					370			375				380				
	Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala	Lys	Asn	Ser	Gly	Tyr	Thr	Ile
20	385					390					395					400
	His	Thr	Ile	Gly	Tyr	Asp	Leu	Gly	Asp	Phe	Ala	Leu	Ala	Asn	Asn	Ser
					405					410					415	
	Leu	Lys	Leu	Thr	Ala	Thr	Asp	Glu	Asn	His	Phe	Phe	Thr	Ala	Thr	Pro
					420				425				430			
25	Ala	Asn	Leu	Ala	Ala	Ala	Phe	Asp	Asn	Ile	Ala	Gln	Thr	Ile	Asn	Ile
					435			440					445			
	Gly	Ile	Gln	Arg	Gly	Glu	Val	Thr	Asp	Phe	Val	Ala	Pro	Gly	Phe	Ile
					450			455				460				
	Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp	Val	Thr	His	Leu	Leu	Asn	Val
30	465					470					475					480
	Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val	Ser	Thr	Lys	Lys	Leu	Thr	Trp
					485					490					495	
	Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser	Glu	Ala	Thr	Ile	Thr	Tyr	Arg
					500				505				510			
35	Ile	Tyr	Ala	Asp	Leu	Asp	Tyr	Ile	Gln	Asn	Asn	Asp	Ile	Pro	Val	Asn
					515			520				525				

	Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly Gly Phe Asp Thr Asn Thr	
	530	535 540
	Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn Gly Glu Pro Asn Gln Gln	
	545	550 555 560
5	Leu Ile Phe Pro Arg Pro Thr Val Lys Leu Gly Tyr Gly Val Ile Lys	
	565	570 575
	Arg His Tyr Val Leu Val Asn Lys Asp Gly Gln Pro Ile Gln Ala Asn	
	580	585 590
	Gly Thr Val Val Ser Ser Leu Ser Glu Ala His Val Leu Gln Ser Gln	
10	595	600 605
	Asp Phe Phe Leu Pro Ser Gly Gly Gly His Ile Val Pro Lys Trp Ile	
	610	615 620
	Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln Tyr Tyr Ser Val Pro Pro	
	625	630 635 640
15	Thr Asn Thr Val Ile Thr Thr Ala Asp Gly Lys Arg Tyr Arg Phe Val	
	645	650 655
	Glu Val Pro Gly Ser Thr Pro Asn Pro Gly Gln Ile Gly Ile Ser Trp	
	660	665 670
	Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala Tyr Lys Leu Leu Asn Tyr	
20	675	680 685
	Trp Met Gly Gly Thr Thr Asp Gln Gln Ser Glu Trp Asp Val Thr Ser	
	690	695 700
	Asn Trp Thr Gly Ala Gln Val Pro Leu Thr Gly Glu Asp Val Glu Phe	
	705	710 715 720
25	Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala Val Ala Asp Leu His Val	
	725	730 735
	Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn Leu Ile Asn Asn Ser Asp	
	740	745 750
	Lys Asp Leu Val Val Thr Thr Ser Ser Gln Leu Thr Ile Asn Gly Val	
30	755	760 765
	Val Glu Asp Asn Asn Pro Asn Val Gly Thr Ile Val Val Lys Ser Ser	
	770	775 780
	Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe Ala Asn Pro Gly Tyr Asn	
	785	790 795 800
35	Gln Asn Val Gly Gly Thr Val Glu Phe Tyr Asn Gln Gly Tyr Asp Cys	
	805	810 815

	Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp Gln Tyr Phe Gly Ile Pro	
	820	825 830
	Val Asn Glu Ser Gly Phe Pro Ile Asn Asp Val Gly Gly Asn Glu Thr	
	835	840 845
5	Val Asn Gln Trp Val Glu Pro Phe Asn Gly Asp Lys Trp Arg Pro Ala	
	850	855 860
	Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys Phe Lys Gly Tyr Gln Ile	
	865	870 875 880
	Thr Asn Asp Val Gln Ala Gln Pro Thr Gly Val Tyr Ser Phe Lys Gly	
10	885	890 895
	Met Ile Cys Val Cys Asp Ala Phe Leu Asn Leu Thr Arg Thr Ser Gly	
	900	905 910
	Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly Asn Ser Tyr Thr Gly Ala	
	915	920 925
15	Ile Asp Ile Lys Gln Gly Ile Val Phe Pro Pro Glu Val Glu Gln Thr	
	930	935 940
	Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp Gln Trp Arg Lys Leu Asn	
	945	950 955 960
	Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly Gln Tyr Leu Ser Val Pro	
20	965	970 975
	Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met	
	980	985 990
	His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk	
	995	1000 1005
25	Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn	
	1010	1015 1020
	Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met	
	1025	1030 1035 1040
	Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu	
30	1045	1050 1055
	Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp	
	1060	1065 1070
	Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr Ala Met	
	1075	1080 1085
35	Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu	
	1090	1095 1100

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Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr
1105          1110          1115          1120
Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu
          1125          1130          1135
5 His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser
          1140          1145          1150
Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu
          1155          1160          1165
Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr
10          1170          1175          1180
Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr
1185          1190          1195          1200
Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val
          1205          1210          1215
15 Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr
          1220          1225          1230
Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu
          1235          1240          1245
Val Glu Tyr
20          1250

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(2) INFORMATION FOR SEQ ID NO:83

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 426 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

    (iii) HYPOTHETICAL: YES

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:

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(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

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	Thr	Met	Glu	Val	Lys	Lys	Asn	Thr	Val	Val	Leu	Arg	Leu	Leu	Ile	Trp
	1				5					10					15	
	Phe	Val	Ala	Ile	Leu	Leu	Phe	His	Ser	Ser	Arg	Leu	Trp	Gly	Gln	Glu
				20				25						30		
10	Gly	Glu	Gly	Ser	Ala	Arg	Tyr	Arg	Phe	Lys	Gly	Phe	Val	Asp	Thr	Tyr
			35				40					45				
	His	Ala	Val	Arg	Ser	Ser	Ser	Pro	Phe	Asp	Phe	Met	Ser	Ser	Arg	Thr
		50					55				60					
	Arg	Val	Arg	Gly	Glu	Leu	Glu	Arg	Ser	Phe	Gly	Asn	Ser	Lys	Val	Ala
15	65				70					75				80		
	Val	Ser	Val	Asn	Ala	Thr	Tyr	Asn	Ala	Leu	Leu	Lys	Asp	Glu	Thr	Gly
				85					90					95		
	Leu	Arg	Leu	Arg	Glu	Ala	Phe	Phe	Glu	His	Gln	Glu	Glu	His	Trp	Gly
				100					105					110		
20	Leu	Arg	Leu	Gly	Arg	Gln	Ile	Val	Ile	Trp	Gly	Ala	Ala	Asp	Gly	Val
				115				120						125		
	Arg	Ile	Thr	Asp	Leu	Ile	Ser	Pro	Met	Asp	Met	Thr	Glu	Phe	Leu	Ala
				130				135					140			
	Gln	Asp	Tyr	Asp	Asp	Ile	Arg	Met	Pro	Val	Asn	Ala	Leu	Arg	Phe	Ser
25	145				150					155				160		
	Val	Phe	Asn	Glu	Ser	Met	Lys	Val	Glu	Val	Val	Val	Leu	Pro	Val	Phe
				165					170					175		
	Glu	Gly	Tyr	Arg	Leu	Pro	Val	Asp	Pro	Arg	Asn	Pro	Trp	Asn	Ile	Phe
				180				185					190			
30	Ser	Leu	Ser	Pro	Ile	Ala	Gln	Gly	Met	Asn	Ile	Val	Trp	Lys	Glu	Glu
				195				200					205			
	Ala	Gly	Lys	Pro	Ala	Phe	Lys	Val	Ala	Asn	Ile	Glu	Tyr	Gly	Ala	Arg
				210				215				220				
	Trp	Ser	Thr	Thr	Leu	Ser	Gly	Ile	Asp	Phe	Ala	Leu	Ala	Ala	Leu	His
35	225				230					235				240		
	Thr	Trp	Asn	Lys	Met	Pro	Val	Ile	Glu	Val	Gln	Gly	Ile	Val	Pro	Thr

		245		250		255										
	Glu	Ile	Ile	Val	Ser	Pro	Arg	Tyr	Tyr	Arg	Met	Gly	Phe	Val	Gly	Gly
		260						265						270		
	Asp	Leu	Ser	Val	Pro	Val	Gly	Gln	Phe	Val	Phe	Arg	Gly	Glu	Ala	Ala
5		275						280					285			
	Phe	Asn	Ile	Asp	Lys	His	Phe	Thr	Tyr	Lys	Ser	His	Ala	Glu	Gln	Glu
		290						295					300			
	Gly	Phe	Gln	Thr	Ile	Asn	Trp	Leu	Ala	Gly	Ala	Asp	Trp	Tyr	Ala	Pro
	305					310					315				320	
10	Gly	Glu	Trp	Met	Ile	Ser	Gly	Gln	Phe	Ser	Met	Glu	Ser	Ile	Phe	Arg
					325					330				335		
	Tyr	Arg	Asp	Phe	Ile	Ser	Gln	Arg	Gln	His	Ser	Thr	Leu	Ile	Thr	Leu
				340				345					350			
	Asn	Val	Ser	Lys	Lys	Phe	Phe	Gly	Ser	Thr	Leu	Gln	Leu	Ser	Asp	Phe
15		355						360					365			
	Thr	Tyr	Tyr	Asp	Leu	Thr	Gly	Lys	Gly	Trp	Phe	Ser	Arg	Phe	Ala	Ala
		370					375					380				
	Asp	Tyr	Ala	Leu	Asn	Asp	Gln	Ile	His	Leu	Met	Ala	Gly	Tyr	Asp	Trp
	385				390					395					400	
20	Phe	Ser	Ser	Lys	Gly	Ser	Gly	Ile	Phe	Asp	Arg	Tyr	Lys	Asp	Asn	Ser
				405						410				415		
	Glu	Leu	Trp	Phe	Lys	Ala	Arg	Tyr	Ser	Phe						
		420					425									

25 (2) INFORMATION FOR SEQ ID NO:84

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

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(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

10	Arg	Gly	Ser	Ser	Ser	Gly	Ile	Ser	Ala	Arg	Gly	Arg	Asp	Met	Arg	Ser	1	5	10	15
	Leu	Phe	Leu	Ser	Ala	Leu	Arg	Ser	Ser	Ser	Leu	His	Gly	Ser	Glu	Arg	20	25	30	
	Arg	Ser	Arg	Ile	Ser	Ser	Ser	Val	Val	Met	Ser	Ile	Arg	Gln	Lys	Ile	35	40	45	
15	Arg	Leu	Phe	His	Leu	Ser	Val	Cys	Ala	Gln	Thr	His	Asp	His	Leu	Ile	50	55	60	
	Glu	Ile	His	Leu	Val	Cys	Ile	Glu	Phe	Gly	Ala	Ile	Asp	Thr	Asp	Glu	65	70	75	80
	Phe	Arg	Leu	Ser	Ser	His	Ala	Tyr	Thr	Thr	Ser	Pro	Thr	His	Thr	Gly	85	90	95	
20	Ala	Ile	His	His	Asn	Cys	Ile	Glu	Arg	Ser	Tyr	Gly	Arg	Tyr	Leu	Val	100	105	110	
	Thr	Phe	Gly	Gln	Glu	Arg	Asn	Glu	Leu	His	His	His	Ser	Arg	Pro	Asp	115	120	125	
25	Arg	Asn	Ala	Glu	Val	Tyr	Arg	Phe	Pro	Phe	Asp	Asn	Ala	Phe	His	Ser	130	135	140	
	Ile	Arg	Tyr	Glu	Ala	Phe	Arg	Pro	Ile	Arg	Pro	Ile	Val	Cys	His	Asp	145	150	155	160
	Asp	His	Phe	Ile	Ala	Ile	Gly	Ser	His	Leu	Phe	Phe	Lys	Asp	Asn	Gln	165	170	175	
30	Ile	Phe	Ser	Ser	Gly	Ser	Gln	Tyr	Asp	Asn	Tyr	Thr	Val	Ala	Cys	Phe	180	185	190	
	Val	Glu	Ser	Leu	His	Asp	Arg	Glu	Gln	Arg	Ser	His	Thr	His	Thr	Ala	195	200	205	
35	Ser	Gly	Thr	Asn	His	Cys	Ala	Asp	Leu	Phe	Asp	Met	Arg	Thr	Leu	Ser	210	215	220	

(2) INFORMATION FOR SEQ ID NO:85

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

Ile	Ile	Tyr	Arg	Ser	Thr	Met	Lys	Leu	Leu	Leu	Tyr	Leu	Leu	Leu	Val
1			5					10			15				
Leu	Ser	Thr	Leu	Ser	Pro	Met	Tyr	Ser	Gln	Met	Leu	Phe	Ser	Glu	Asn
20				25				30							
Leu	Thr	Met	Asn	Ile	Asp	Ser	Thr	Lys	Thr	Ile	Gln	Gly	Thr	Ile	Leu
35			40				45								
Pro	Val	Leu	Asp	Phe	Lys	Thr	Glu	Lys	Glu	Asn	Val	Phe	Thr	Phe	Lys
50			55				60								
Asn	Thr	Ala	Asn	Leu	Asn	Leu	Leu	Ile	Lys	His	Gly	Gln	Val	Ile	Asn
65			70				75				80				
Leu	Ile	Asn	Lys	Leu	Glu	Phe	Ser	Thr	Tyr	Gly	Asn	Lys	Val	Thr	Val

	85	90	95
	Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val		
	100	105	110
	Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly		
5	115	120	125
	Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val		
	130	135	140
	Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu		
	145	150	155
10	Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr		
	165	170	175
	Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His		
	180	185	190
	Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly		
15	195	200	205
	Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp		
	210	215	220
	Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg		
	225	230	235
20	Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn		
	245	250	255
	Thr Val Asp Val Gly Ile Asp Ile Ser Phe		
	260	265	

25 (2) INFORMATION FOR SEQ ID NO:86

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

5

(B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

```

10  Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys
    1          5          10          15
    Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu Thr Gly
        20          25          30
    Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr Ala Phe
        35          40          45
15  Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser Ala Tyr
    50          55          60
    Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Gly Ser Ile Thr Arg
    65          70          75          80
    Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu Asn Leu
20          85          90          95
    Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg Trp Met
        100          105          110
    Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn Pro Ala
        115          120          125
25  Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala Ala Ala
    130          135          140
    Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met Asp Asn
    145          150          155          160
    Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly Gly Ile
30          165          170          175
    Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu Tyr Thr
        180          185          190
    Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser Glu Thr
        195          200          205
35  Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe Gly Ile
    210          215          220

```

Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe Leu Leu
 225 230 235 240
 Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly Lys Phe
 245 250 255
 5 Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg Asn Phe
 260 265 270
 Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser Ser Leu
 275 280 285
 Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile Gly Phe
 10 290 295 300
 Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn Thr Gly
 305 310 315 320
 Arg Arg Thr Ser Leu Tyr Tyr His Asp
 325

15

(2) INFORMATION FOR SEQ ID NO:87

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 amino acids
 20 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

30 (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

35

Pro Arg Phe His Pro Gly Gly Thr His Ala Gln Leu Cys Arg Asn Gly

	1		5		10		15									
	Arg	Arg	Asn	Gln	Lys	Ser	Asn	Gln	Ser	Ser	Cys	Phe	Gly	Gly	Gly	Thr
			20				25						30			
	Ala	Pro	Arg	Phe	Phe	Ile	Met	Cys	Lys	Ile	Arg	Phe	Ser	Leu	Leu	Gln
5		35					40					45				
	Ala	Leu	Val	Val	Cys	Leu	Leu	Phe	Thr	Ser	Phe	Ser	Leu	Gln	Ala	Gln
		50					55					60				
	Glu	Glu	Gly	Ile	Trp	Asn	Thr	Leu	Leu	Ala	Ile	His	Lys	Thr	Glu	Lys
	65					70					75				80	
10	Ala	Val	Glu	Thr	Pro	Lys	Lys	Val	Phe	Ala	Val	Ala	Asn	Gly	Val	Leu
						85					90				95	
	Tyr	Ser	Val	Gly	Lys	Glu	Ala	Pro	His	Glu	Ala	Lys	Ile	Phe	Asp	Arg
			100						105					110		
	Ile	Ser	Gly	Leu	Ser	Asp	Thr	Ser	Val	Ser	Ser	Ile	Ala	Tyr	Ser	Glu
15		115					120					125				
	Gln	Leu	Lys	Ser	Leu	Val	Ile	Tyr	Tyr	Ala	Ser	Gly	Asn	Ile	Asp	Ile
		130					135					140				
	Leu	Asp	Glu	Ala	Gly	Arg	Val	Thr	Asn	Val	Pro	Ala	Leu	Lys	Asp	Asn
	145					150					155				160	
20	Ile	Asp	Leu	Ile	Asp	Lys	Thr	Leu	Asn	Arg	Leu	Leu	Ile	Val	Gly	Asn
						165				170				175		
	Arg	Ala	Tyr	Leu	Ala	Gly	Gly	Phe	Gly	Leu	Ser	Val	Leu	Asp	Val	Ala
			180						185				190			
	Glu	Ala	Arg	Ile	Pro	Ala	Thr	Tyr	Ala	Lys	Gly	Thr	Lys	Val	Thr	Asp
25		195					200					205				
	Val	Ala	Lys	Leu	Asp	Asn	Asp	Arg	Leu	Leu	Met	Leu	Lys	Glu	Gly	Gln
		210					215					220				
	Leu	Phe	Ile	Gly	Lys	Glu	Thr	Asp	Asn	Leu	Gln	Asp	Pro	Ala	Ala	Trp
	225				230					235					240	
30	Thr	Ala	Leu	Ser	Leu	Asn	Leu	Pro	Met	Gly	Ser	Val	Thr	Gly	Leu	Gly
						245				250				255		
	Ile	Val	Gly	Glu	Asp	Ile	Cys	Phe	Leu	Leu	Ala	Asp	Gly	Arg	Val	Tyr
			260					265				270				
	Val	Ala	Ala	Asn	Gln	Ser	Phe	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Ser	Ser
35		275						280					285			
	Ala	Asp	Ser	Arg	Leu	Tyr	Val	Thr	Asp	Arg	Gly	Leu	Phe	Ile	Cys	Ala

	290		295		300
	Glu Asn Arg Ile Tyr Phe Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe				
	305		310		315
	Pro Ile Ala Asp Val Leu Gly Val Gly Ala Met Asn Glu Ser Asn Thr				
5		325		330	335
	Ala Tyr Ile Ala Leu Gly Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala				
		340		345	350
	Glu Gly Ser Thr Ala Glu Ala Met Pro Val Ala Phe Asp Gly Pro Gly				
		355		360	365
10	Asp Asn Asp Phe Tyr Glu Met Arg Phe Ser His Gly Arg Leu Tyr Ala				
		370		375	380
	Ala Ser Gly Leu Trp Gly Thr Asn Leu Met Gly His Ala Gly Met Val				
		385		390	395
	Lys Leu Tyr Asp Gly Asn Arg Trp Thr Asn Phe Asp Lys Lys Thr Val				
15		405		410	415
	Gln Glu Gln Leu Gly Gly Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile				
		420		425	430
	Ala Val Ser Asn Gly Asp Pro Asp His Phe Phe Val Gly Thr Trp Gly				
		435		440	445
20	Asn Gly Leu Phe Glu Phe Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser				
		450		455	460
	Gly Asn Glu Thr Ala Ile Ala Glu Cys Asn Pro Gly Asp Ala Arg Val				
		465		470	475
	Lys Ala Ile Ala Phe Asp Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly				
25		485		490	495
	Ala Val Gly Lys Asn Ile Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp				
		500		505	510
	His Ser Phe Ser Tyr Pro Asp Val Ala Asn Leu Ala Ser Phe Gly Asn				
		515		520	525
30	Met Ile Ile Leu Pro Asn Gly Asp Lys Trp Val Asn Ile Leu His Arg				
		530		535	540
	Ser Gly Gly Ser Thr Arg Lys Gly Val Leu Ile Phe Asn Asp Arg Gly				
		545		550	555
	Thr Pro Glu Thr Thr Ser Asp Asp Ser His Leu Tyr Val Glu Gln Phe				
35		565		570	575
	Val Asn Arg Leu Gly Ala Ala Ile Gly His Lys Thr Ile Tyr Ala Met				

30

(2) INFORMATION FOR SEQ ID NO:88

(i) SEQUENCE CHARACTERISTICS:

- 35

(A) LENGTH: 451 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

10

(A) NAME/KEY: misc_feature

(B) LOCATION 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

```

15  Lys Thr Ser Tyr Arg Asn Asn Met Arg Phe Gln His Tyr Leu Ile Cys
    1             5             10             15
    Thr Ala Ala Val Ala Ala Leu Ala Ala Asn Pro Leu Thr Gly Gln Ser
        20             25             30
    Asn Met Thr Leu Glu Glu Cys Ile Asp Tyr Ala Arg Arg His Ser Ser
20             35             40             45
    Ala Val Ala Leu Ser Ala Ala Glu Leu Glu Gln Ser Lys Ala Asp Tyr
        50             55             60
    Leu Gln Ala Val Gly Asn Phe Leu Pro Arg Val Ser Ala Gly Thr Gly
    65             70             75             80
25  Ala Ser Trp Asn Phe Gly Arg Gly Leu Asp Ala Glu Thr Asn Thr Tyr
        85             90             95
    Thr Asp Ile Asn Ser Phe Asn Asn Ser Tyr Ser Ile His Ala Thr Met
        100            105            110
    Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His
30             115            120            125
    Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Glu Leu
        130            135            140
    Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg
    145            150            155            160
35  Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu
        165            170            175

```

His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro
 180 185 190
 Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu
 195 200 205
 5 Thr Gln Ala Asp Asn Gln Cys Ile Ile Ala Leu Ile Arg Leu Lys Glu
 210 215 220
 Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro
 225 230 235 240
 Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ser Ala Gly
 10 245 250 255
 Val Phe Ala Arg Ala Ala His His His Pro Val Leu Leu Arg Ala Lys
 260 265 270
 Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala
 275 280 285
 15 Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser
 290 295 300
 Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg
 305 310 315 320
 Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe
 20 325 330 335
 Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg
 340 345 350
 Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser
 355 360 365
 25 Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Ala Leu Ala Ser Tyr
 370 375 380
 Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala
 385 390 395 400
 Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr
 30 405 410 415
 Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala
 420 425 430
 Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys
 435 440 445
 35 Leu Ser Asp
 450

(2) INFORMATION FOR SEQ ID NO:89

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 834 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...834

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

Met Lys Arg Ile Val Leu Ser Ser Phe Leu Phe Val Leu Ser Ile Leu
 1 5 10 15
 Ser Leu Met Ala Gln Asn Asn Thr Leu Asp Val His Ile Ser Gly Thr
 25 20 25 30
 Ile Lys Asp Ala Ser Ser Gly Glu Pro Val Pro Tyr Ala Thr Val Ser
 35 40 45
 Ile Arg Leu Thr Gly Ala Asp Thr Thr Gln Val Phe Arg Gln Val Thr
 50 55 60
 30 Asp Gly Asn Gly Tyr Phe Val Ile Gly Leu Pro Ala Ala Pro Ser Tyr
 65 70 75 80
 His Leu Thr Ala Ser Phe Val Gly Met Lys Thr His Thr Met Gln Ile
 85 90 95
 Ser Arg Gly Asn Gly Gln His Asp Ile Lys Ser Ile Asp Ile Ser Leu
 35 100 105 110
 Glu Ser Glu Asp Lys Gln Leu Ser Thr Val Thr Val Ser Ala Ala Arg

	115		120		125
	Pro Leu Val Lys Met Glu Ile Asp Arg Leu Ser Tyr Asn Met Lys Asp				
	130		135		140
	Asp Pro Ala Ala Lys Thr Asn Asn Leu Leu Glu Met Leu Arg Asn Val				
5	145		150		155
	Pro Leu Val Thr Val Asp Gly Gln Gly Asn Ile Gln Val Lys Gly Ser				
		165		170	175
	Ser Asn Phe Lys Ile His Leu Asn Gly Arg Pro Ser Thr Met Val Ser				
		180		185	190
10	Ser Asn Pro Lys Glu Val Phe Arg Ser Ile Pro Ala His Thr Ile Lys				
		195		200	205
	Arg Val Glu Val Ile Thr Asp Pro Gly Val Lys Tyr Asp Ala Glu Gly				
		210		215	220
	Thr Ser Ala Ile Leu Asp Ile Val Thr Glu Glu Gly Lys Lys Leu Glu				
15	225		230		235
	Gly Tyr Ser Gly Ser Ile Thr Ala Ser Val Ser Asn Asn Pro Thr Ala				
		245		250	255
	Asn Gly Ser Ile Phe Leu Thr Ala Lys Ser Gly Lys Val Gly Leu Thr				
		260		265	270
20	Thr Asn Tyr Asn Tyr Tyr Gly Gly Lys Asn Lys Gly Ser Arg Tyr Phe				
		275		280	285
	Thr Glu Arg Thr Thr Ser Met Leu Gln Thr Ile Glu Glu Gly Lys Gly				
		290		295	300
	Gln Glu Thr Phe Gly Gly His Phe Gly Asn Ala Leu Leu Ser Phe Glu				
25	305		310		315
	Ile Asp Ser Leu Asn Leu Phe Thr Val Gly Gly Asn Val Arg Leu Trp				
		325		330	335
	Glu Met Thr Thr Asp Arg Asn Ser Val Glu Lys Ser Phe Ala Gly Ser				
		340		345	350
30	Asn Leu Met Ser Tyr Ile Asp Arg Lys Leu Lys Thr Gln Met Asp Ala				
		355		360	365
	Gly Ser Tyr Glu Leu Asn Ala Asp Tyr Gln His Ser Thr Arg Leu Pro				
		370		375	380
	Gly Glu Leu Leu Thr Val Ser Tyr Arg Phe Thr His Asn Pro Asn Asn				
35	385		390		395
	Ser Glu Thr Phe Ile Asp Gln Trp Lys Arg Asp Pro Leu Asn Thr Ala				
					400

		405		410		415										
	Asn	Thr	Ile	Gln	Tyr	Ala	Gly	Gln	His	Ser	Lys	Ser	Asp	Ala	Gly	Met
		420		425		430										
	Asp	Glu	His	Thr	Ala	Gln	Val	Asp	Tyr	Thr	Arg	Pro	Leu	Gly	Gln	Ala
5		435		440		445										
	His	Ser	Leu	Glu	Ala	Gly	Leu	Lys	Tyr	Ile	Tyr	Arg	His	Ala	Thr	Ser
		450		455		460										
	Asp	Pro	Leu	Tyr	Glu	Ile	Arg	Pro	Ser	Glu	Asp	Ala	Pro	Trp	Gln	Pro
	465			470		475									480	
10	Gly	Ser	Leu	Tyr	Ala	Gln	Asn	Pro	Ser	Asn	Gly	Lys	Phe	Arg	His	Asp
				485		490									495	
	Gln	Tyr	Ile	Gly	Ala	Ala	Tyr	Ala	Gly	Tyr	Asn	Tyr	Arg	Lys	Asp	Gln
				500		505									510	
	Tyr	Ser	Leu	Gln	Thr	Gly	Leu	Arg	Val	Glu	Ser	Ser	Arg	Leu	Lys	Ala
15		515		520		525										
	Leu	Phe	Pro	Glu	Asn	Ala	Ala	Ala	Asp	Phe	Ser	His	Asn	Ser	Phe	Asp
		530		535		540										
	Trp	Val	Pro	Gln	Leu	Thr	Leu	Gly	Tyr	Thr	Pro	Ser	Pro	Met	Lys	Gln
	545			550		555									560	
20	Leu	Lys	Leu	Ala	Tyr	Asn	Phe	Arg	Ile	Gln	Arg	Pro	Ala	Ile	Gly	Gln
				565		570									575	
	Leu	Asn	Pro	Tyr	Arg	Leu	Gln	Thr	Asn	Asp	Unk	Gln	Val	Gln	Tyr	Gly
				580		585									590	
	Asn	Pro	Asp	Leu	Lys	Ser	Glu	Lys	Arg	His	His	Val	Gly	Leu	Ser	Tyr
25		595		600		605										
	Asn	Gln	Tyr	Gly	Ala	Lys	Val	Met	Leu	Thr	Ala	Ser	Leu	Asp	Tyr	Asp
		610		615		620										
	Phe	Cys	Asn	Asn	Ala	Ile	Gln	Asn	Tyr	Thr	Phe	Ser	Asp	Pro	Ala	Asn
	625			630		635									640	
30	Pro	Asn	Leu	Phe	His	Gln	Thr	Tyr	Gly	Asn	Ile	Gly	Arg	Glu	His	Ser
				645		650									655	
	Phe	Ser	Leu	Asn	Thr	Tyr	Ala	Met	Tyr	Thr	Pro	Ala	Val	Trp	Val	Arg
				660		665									670	
	Ile	Met	Leu	Asn	Gly	Asn	Ile	Asp	Arg	Thr	Phe	Gln	Lys	Ser	Glu	Ala
35		675		680		685										
	Leu	Gly	Ile	Asp	Val	Asn	Ser	Trp	Ser	Gly	Met	Val	Tyr	Ser	Gly	Leu

	690		695		700											
	Met	Phe	Thr	Leu	Pro	Lys	Asp	Trp	Thr	Val	Asn	Leu	Phe	Gly	Gly	Tyr
	705					710					715					720
	Tyr	His	Gly	Gly	Arg	Ser	Tyr	Gln	Thr	Lys	Tyr	Asp	Gly	Asn	Val	Phe
5					725					730						735
	Asn	Asn	Ile	Gly	Ile	Ala	Lys	Gln	Leu	Phe	Asp	Lys	Lys	Leu	Arg	Val
				740						745						750
	Ser	Leu	Ser	Ala	Asn	Asn	Ile	His	Ala	Lys	Tyr	Ser	Thr	Trp	Lys	Ser
				755						760						765
10	Arg	Thr	Ile	Gly	Asn	Gly	Phe	Thr	Ile	Tyr	Ser	Glu	Asn	Ala	Gly	Ile
				770						775						780
	Gln	Arg	Ser	Val	Ser	Leu	Ser	Leu	Thr	Tyr	Ser	Phe	Gly	Lys	Met	Asn
						785										790
	Thr	Gln	Val	Arg	Lys	Val	Glu	Arg	Thr	Ile	Val	Asn	Asp	Asp	Leu	Lys
15						805										810
	Gln	Thr	Ser	Ser	Gln	Gly	Gln	Gln	Gly	Gly	Gly	Gln	Gly	Asn	Pro	Thr
						820										825
																830
	Gly	Asn														

20

(2) INFORMATION FOR SEQ ID NO:90

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 593 amino acids
25	(B) TYPE: amino acid
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

5	Met	Asn	Ser	Ile	Met	Lys	Tyr	Gln	Leu	Tyr	Thr	Ala	Val	Ile	Met	Ala
	1				5				10					15		
	Leu	Ser	Val	Ser	Ser	Val	Cys	Gly	Gln	Thr	Pro	Arg	Asn	Thr	Glu	Thr
				20					25					30		
	Lys	Arg	Pro	Asp	Thr	Leu	Arg	Arg	Glu	Leu	Thr	Ile	Val	Asn	Asp	Gln
10			35					40					45			
	Thr	Val	Glu	Met	Glu	His	Ala	Asp	Pro	Leu	Pro	Ala	Ala	Tyr	Lys	Ala
			50				55					60				
	Ile	Glu	Pro	Arg	Leu	Lys	Pro	Phe	Arg	Pro	Glu	Tyr	Asn	Lys	Arg	Thr
	65				70				75					80		
15	Phe	Gly	Phe	Val	Pro	Glu	Val	Ser	Ser	Ser	Gly	Arg	Asn	Asn	Leu	Pro
				85					90					95		
	Asn	Ile	Leu	Pro	Thr	Glu	Gly	His	Met	Lys	His	Arg	Gly	Tyr	Leu	Asn
				100					105					110		
	Ile	Gly	Ile	Gly	His	Thr	Leu	Asn	Gln	Arg	Met	Asp	Ala	Gly	Tyr	Arg
20				115					120					125		
	Leu	Ile	Asp	Ala	Glu	Gln	Glu	Arg	Leu	Asn	Leu	Phe	Leu	Ser	Tyr	Arg
			130				135					140				
	Gly	Met	Lys	Ser	Ala	Phe	Asn	Thr	Gly	Asp	Phe	Asp	Gly	Asp	Arg	Lys
	145				150				155					160		
25	Asp	Arg	Arg	Met	Met	Ala	Gly	Val	Asp	Tyr	Glu	Gln	Arg	Arg	Pro	Ser
				165					170					175		
	Phe	Val	Leu	Ala	Thr	Gly	Leu	Tyr	Tyr	Ser	Asn	His	Tyr	Phe	Asn	Asn
				180					185					190		
	Tyr	Gly	Arg	Gly	Ala	Thr	Thr	Asn	Val	Gly	Ser	Ile	Pro	Gln	Leu	Ser
30				195					200					205		
	Thr	Pro	Val	Thr	Pro	Gln	Met	Asp	Asn	Gly	Thr	His	Asn	Val	Arg	Val
				210			215					220				
	Tyr	Leu	Gly	Ala	Lys	Asn	Asp	Val	Ile	Asp	Ala	Arg	Ile	Asp	Tyr	Arg
	225				230				235					240		
35	Phe	Phe	Arg	Ser	Ile	Pro	Tyr	Leu	Gly	Thr	Asp	Pro	Met	Lys	Ala	Leu
				245					250					255		

	Thr	Glu	His	Thr	Pro	Glu	Leu	Asn	Val	Thr	Met	Ser	Asn	Glu	Leu	Ser	
					260					265						270	
	Asp	Asp	Ile	Lys	Leu	Gly	Val	Glu	Val	Arg	Thr	Gly	Gly	Leu	Phe	Phe	
					275					280						285	
5	Ala	Lys	Asn	Ser	Glu	Met	Ile	Gln	Thr	Gly	Val	Leu	Ser	Glu	Thr	Asp	
					290					295						300	
	Arg	Asn	Leu	Tyr	Tyr	Val	Glu	Gly	Ala	Pro	Thr	Ile	Gly	Phe	Val	Gly	
					305					310						315	
	Asp	Ser	Asp	Asn	Met	Gln	Trp	Asn	Ile	Gln	Ala	Gly	Val	Gly	Ile	Ser	
10					325					330						335	
	Ser	His	Phe	Gly	Ala	Lys	Gly	Arg	Leu	Phe	Phe	Trp	Pro	Lys	Leu	Asp	
					340					345						350	
	Ala	Ser	Leu	Ser	Ile	Phe	Pro	Ser	Trp	Arg	Val	Tyr	Ala	Lys	Ala	Phe	
					355					360						365	
15	Gly	Gly	Val	Ile	Arg	Asn	Gly	Leu	Ala	Asp	Val	Met	Gln	Glu	Glu	Met	
					370					375						380	
	Pro	Tyr	Leu	Met	Pro	Asn	Thr	Ile	Val	Leu	Pro	Ser	Arg	Asn	Ala	Leu	
					385					390						395	
	Thr	Ala	Gln	Leu	Gly	Val	Lys	Gly	Asn	Ile	Ala	Asp	Val	Val	Arg	Met	
20					405					410						415	
	Glu	Val	Tyr	Gly	Asp	Phe	Ser	Lys	Leu	Thr	Gly	Val	Pro	Phe	Tyr	Thr	
					420					425						430	
	Pro	Thr	Leu	Pro	Leu	Tyr	Asn	Pro	Ser	Asp	Leu	Tyr	Gln	Tyr	Asn	Val	
					435					440						445	
25	Ser	Phe	Leu	Pro	Ile	Tyr	Ala	Asp	Gly	Ser	Arg	Trp	Arg	Ala	Gly	Gly	
					450					455						460	
	Lys	Leu	Glu	Tyr	Ser	Tyr	Arg	Asp	Met	Leu	Arg	Phe	Leu	Val	Asp	Ala	
					465					470						475	
	Ser	Tyr	Gly	Lys	Trp	Asn	Leu	Asp	Gly	Gly	Leu	Val	Ala	Ser	Met	Gln	
30					485					490						495	
	Pro	Asp	Leu	Ile	Leu	Lys	Ala	Glu	Val	Gly	Val	His	Pro	Ile	Ala	Pro	
					500					505						510	
	Leu	Asp	Val	Arg	Leu	Arg	Tyr	Thr	Gln	Leu	Asn	Gly	Arg	Tyr	Arg	Tyr	
					515					520						525	
35	Ser	Phe	Gly	Ser	Ala	Gly	Ser	Glu	Ala	Leu	Gly	Ile	Gly	Asn	Val	His	
					530					535						540	

Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu
 545 550 555 560
 Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly
 565 570 575
 5 Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr
 580 585 590
 Phe

10 (2) INFORMATION FOR SEQ ID NO:91

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 589 amino acids

 (B) TYPE: amino acid

15 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

20

 (vi) ORIGINAL SOURCE:

 (A) ORGANISM: *Porphyromonas gingivalis*

 (ix) FEATURE:

25 (A) NAME/KEY: misc_feature

 (B) LOCATION 1...589

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

30 Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser
 1 5 10 15
 Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp
 20 25 30
 Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met
 35 35 40 45
 Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg

	50		55		60	
	Leu Lys Pro Phe Arg	Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val				
	65	70	75	80		
	Pro Glu Val Ser Ser Ser	Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro				
5	85	90	95			
	Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly					
	100	105	110			
	His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala					
	115	120	125			
10	Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser					
	130	135	140			
	Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg Met					
	145	150	155	160		
	Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu Ala					
15	165	170	175			
	Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg Gly					
	180	185	190			
	Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val Thr					
	195	200	205			
20	Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly Ala					
	210	215	220			
	Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg Ser					
	225	230	235	240		
	Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His Thr					
25	245	250	255			
	Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile Lys					
	260	265	270			
	Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn Ser					
	275	280	285			
30	Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu Tyr					
	290	295	300			
	Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp Asn					
	305	310	315	320		
	Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe Gly					
35	325	330	335			
	Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu Ser					

(2) INFORMATION FOR SEQ ID NO:92

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 amino acids

(D) TOPOLOGY: linear

5

(vi) ORIGINAL SOURCE:

10

(A) NAME/KEY: misc feature

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

1 5 10 15

20

20 25 30

35 40 45

50 55 60

65 70 75 80

85 90 95

30

100 105 110

115 120 125

130 135 140

145 150 155 160

Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
 165 170 175
 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
 180 185 190
 5 Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
 195 200 205
 Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
 210 215 220
 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
 10 225 230 235 240
 Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
 245 250 255
 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
 260 265 270
 15 Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
 275 280 285
 Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
 290 295 300
 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
 20 305 310 315 320
 Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
 325 330

(2) INFORMATION FOR SEQ ID NO:93

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...229

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

```

Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser
1           5           10           15
10 Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr
           20           25           30
Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro
           35           40           45
Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro
15           50           55           60
Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile
65           70           75           80
Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp
           85           90           95
20 Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe
           100          105          110
Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg
           115          120          125
Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro
25           130          135          140
Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile
145          150          155          160
Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr
           165          170          175
30 Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe
           180          185          190
Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr
           195          200          205
Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr
35           210          215          220
Val Ser Gln Gln Lys

```

225

(2) INFORMATION FOR SEQ ID NO:94

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser Ser
 1 5 10 15
 25 Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe
 20 25 30
 Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val
 35 40 45
 Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe
 30 50 55 60
 Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala
 65 70 75 80
 Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys
 85 90 95
 35 Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp
 100 105 110

Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile
 115 120 125
 Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys
 130 135 140
 5 Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg
 145 150 155 160
 Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe
 165 170 175
 Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu
 10 180 185 190
 Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr Ala
 195 200 205
 Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val
 210 215 220
 15 Ser Gln Gln Lys
 225

(2) INFORMATION FOR SEQ ID NO:95

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 547 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- 30 (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...547
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

	Met	Lys	Thr	Ile	Val	Arg	Tyr	Ser	Arg	Leu	Pro	Val	Ala	Leu	Phe	Phe
	1				5					10					15	
	Cys	Leu	Leu	Gly	Ala	Val	His	Leu	Ser	Val	Glu	Ala	Gln	Met	Leu	Asn
5				20					25					30		
	Thr	Pro	Phe	Glu	Leu	Ser	Asp	Gln	Ile	Val	Leu	Ser	Pro	Thr	Glu	Arg
				35					40					45		
	Gln	Tyr	Arg	Glu	Ile	Cys	Val	Gln	Thr	Lys	Glu	Lys	Arg	Gly	Ala	Asp
				50				55					60			
10	Leu	Phe	Pro	Leu	Ser	Asp	Lys	Leu	Arg	Asp	Ser	Ala	Tyr	Val	Arg	Phe
	65					70					75				80	
	Gly	Ser	Ala	Tyr	Gly	Asp	Ile	Ala	Gly	Asp	Tyr	Leu	Pro	Tyr	Asn	Gly
					85					90					95	
	Asn	Asn	Tyr	Ser	Ser	Leu	Ser	Leu	Glu	Ser	Gly	Gly	Arg	Ile	Ser	Val
15				100					105					110		
	Arg	Asn	Tyr	Gly	Thr	Leu	Gln	Gly	Ser	Ala	Ser	Tyr	Ser	Arg	Gly	Met
				115					120					125		
	His	Lys	Arg	Ile	Gly	Trp	Asn	Ala	Leu	Arg	Asn	Ala	Glu	Ala	Tyr	Tyr
				130				135					140			
20	Pro	Tyr	Leu	Val	Ser	Asp	Ser	Thr	Gly	Gly	Asp	Tyr	His	Phe	Glu	Asp
	145					150					155				160	
	Tyr	Arg	Leu	Ala	Gly	Tyr	Tyr	Ser	Phe	Arg	Ala	Gly	Arg	Leu	Pro	Leu
				165					170					175		
	Gly	Ile	Gly	Phe	Ser	Tyr	Arg	Gly	Glu	Val	Ala	Tyr	Arg	Leu	Thr	Asp
25				180					185					190		
	Pro	Arg	Thr	Thr	Asn	Thr	Thr	Gly	Ala	Leu	Glu	Leu	Ser	Cys	Ala	Thr
				195					200					205		
	Ser	Leu	Thr	Leu	Pro	Arg	Glu	Asn	Arg	Leu	Ser	Leu	Ser	Ala	Ala	Tyr
				210				215						220		
30	Leu	Tyr	His	Arg	Gln	His	Leu	Thr	Gln	Tyr	Asn	Trp	Arg	Pro	Gly	Gln
	225					230					235				240	
	Gln	Asp	Lys	Phe	Phe	Val	Ser	Tyr	Gly	Phe	Gly	Gln	Val	Asp	Val	Ser
				245						250				255		
	Asn	Ser	Pro	Ile	Trp	Phe	Gly	Ile	Ser	Arg	Met	Asn	Tyr	Val	Asn	Gly
35				260					265					270		
	Trp	Lys	Leu	Ser	Ser	Arg	Leu	Asp	Thr	Arg	Arg	Gly	Asp	Ala	Ile	Gly

	275		280		285
	Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg Ser Ser Ile				
	290		295		300
	Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr Gly Ser Trp				
5	305		310		315 320
	His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr Ala Leu Arg				
		325		330	335
	Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp Asp Asn Tyr				
		340		345	350
10	His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp Tyr Met Leu				
		355		360	365
	Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile Arg Thr Asp				
		370		375	380
	Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe Tyr Gly Tyr				
15	385		390		395 400
	Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser Gly Met Leu				
		405		410	415
	Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser Lys Leu Asp				
		420		425	430
20	Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu Thr His Ser				
		435		440	445
	Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr Gln Leu Ala				
		450		455	460
	Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu Val Arg Ser				
25	465		470		475 480
	Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr				
		485		490	495
	Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala				
		500		505	510
30	Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln				
		515		520	525
	Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser				
		530		535	540
	Tyr Leu Phe				
35	545				

(2) INFORMATION FOR SEQ ID NO:96

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

20

Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys
 1 5 10 15
 Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser
 20 25 30
 25 Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala
 35 40 45
 Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys
 50 55 60
 Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser
 30 65 70 75 80
 Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe
 85 90 95
 Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly
 100 105 110
 35 Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met
 115 120 125

	Pro	Asp	Phe	Ala	Ser	Ser	Ile	Glu	Asp	Leu	Gln	Val	Gln	Arg	Gly	Val	
	130						135					140					
	Gly	Thr	Ser	Thr	Asn	Gly	Ala	Gly	Ala	Phe	Gly	Ala	Ser	Val	Asn	Met	
	145					150					155					160	
5	Arg	Thr	Asp	Asn	Leu	Gly	Leu	Ala	Pro	Tyr	Gly	Arg	Val	Asp	Leu	Ser	
					165					170					175		
	Gly	Gly	Ser	Phe	Gly	Thr	Phe	Arg	Arg	Ser	Val	Lys	Leu	Gly	Ser	Gly	
				180					185					190			
	Arg	Ile	Gly	Arg	His	Trp	Ala	Val	Asp	Ala	Arg	Leu	Ser	Lys	Ile	Gly	
10			195					200					205				
	Ser	Asp	Gly	Tyr	Val	Asp	Arg	Gly	Ser	Val	Asp	Leu	Lys	Ser	Tyr	Phe	
	210						215					220					
	Ala	Gln	Val	Gly	Tyr	Phe	Gly	Ser	Asn	Thr	Ala	Leu	Arg	Phe	Ile	Thr	
	225					230					235					240	
15	Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp	Asn	Gly	Leu	Ser	Lys	
				245						250					255		
	Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn	Ser	Ala	Gly	Leu	Met	
			260					265					270				
	Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr	His	Asn	Thr	Asp	Asn	
20			275					280					285				
	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr	His	Ser	Phe	Ser	Pro	
	290						295					300					
	Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr	
	305				310						315					320	
25	Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys	Glu	Tyr	Ala	Leu	Gln	
				325						330					335		
	Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys	Thr	Asp	Leu	Ile	Arg	
			340					345					350				
	Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu	Ile	Gly	Ser	Leu	Asn	
30			355					360					365				
	Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly	Ala	Ser	Gly	Asn	Ile	
	370					375					380						
	Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr	Ile	Lys	Lys	Tyr	Asn	
	385				390						395					400	
35	Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg	Asn	Arg	Ala	Asp	Lys	
				405						410					415		

	Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp	Gln	Ile	Thr	Pro	Glu	
				420					425						430		
	Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr	Ile	Gly	Tyr	Thr	Ile	
			435					440					445				
5	Asn	Gly	Ile	Thr	Asp	Glu	Tyr	Asp	Glu	Val	Gln	Gly	Ser	Met	Gln	His	
		450				455					460						
	Ile	Asp	Leu	Asp	Lys	Thr	Phe	Arg	Phe	Leu	Asn	Pro	Lys	Ala	Gly	Leu	
	465					470					475				480		
	Thr	Tyr	Ser	Phe	Asp	Asp	Ala	His	Thr	Ala	Tyr	Ala	Ser	Val	Ala	Val	
10				485						490				495			
	Ala	His	Arg	Glu	Pro	Asn	Arg	Thr	Asn	Tyr	Thr	Glu	Ala	Gly	Ile	Gly	
				500					505					510			
	Gln	Tyr	Pro	Thr	Pro	Glu	Arg	Leu	Ile	Asp	Tyr	Glu	Leu	Gly	Tyr	Arg	
			515					520						525			
15	Tyr	Ala	Ser	Pro	Leu	Leu	Ser	Ala	Gly	Val	Gly	Leu	Tyr	Tyr	Met	Gln	
		530					535					540					
	Tyr	Lys	Asp	Gln	Leu	Val	Leu	Asp	Gly	Arg	Leu	Ser	Asp	Val	Gly	Gln	
	545					550					555				560		
	Met	Leu	Thr	Ser	Asn	Val	Pro	Asp	Ser	Tyr	Arg	Met	Gly	Leu	Glu	Leu	
20				565						570				575			
	Thr	Leu	Gly	Trp	Gln	Ile	Leu	Pro	Arg	Leu	Leu	Arg	Trp	Asp	Ala	Ser	
				580						585				590			
	Phe	Thr	Met	Ser	Arg	Asn	Lys	Ile	Asp	Arg	Tyr	Val	Gln	Tyr	Thr	Ser	
			595				600						605				
25	Val	Tyr	Asp	Ala	Asp	Tyr	Asn	Trp	Leu	Glu	Leu	Lys	Glu	Glu	Thr	Leu	
		610					615					620					
	Glu	Ser	Thr	Asp	Ile	Ala	Tyr	Ser	Pro	Asn	Val	Ile	Ala	Gly	Ser	Met	
	625					630					635				640		
	Leu	Thr	Leu	Ser	His	Ala	Gly	Phe	Glu	Met	Ala	Trp	Thr	Ser	Arg	Phe	
30				645						650				655			
	Val	Ser	Lys	Gln	Tyr	Leu	Asp	Asn	Thr	Gln	Arg	Ser	Asp	Arg	Met	Leu	
				660						665				670			
	Ser	Ser	Tyr	Trp	Val	Asn	Asp	Leu	Arg	Leu	Gly	Tyr	Val	Leu	Pro	Val	
			675					680					685				
35	His	Phe	Val	Lys	Arg	Val	Ala	Leu	Gly	Val	Gln	Leu	Asn	Asn	Leu	Phe	
		690						695					700				

```

Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr Asp Ala Gly Tyr Val
705              710              715              720
Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp Leu Arg Tyr Tyr Pro
              725              730              735
5  Gln Ala Gly Phe Asn Ala Leu Gly Unk Leu Thr Ile Asp Phe
              740              745              750

```

(2) INFORMATION FOR SEQ ID NO:97

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...285

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

```

Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val Val Arg
1              5              10              15
30 Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val Ser Ala
              20              25              30
Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys Asp Thr
              35              40              45
Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg Val Ala
35      50              55              60
Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His Ala Ser

```

	65		70		75		80									
	Ser	Ile	His	Val	Ala	Val	Arg	Thr	Asp	Phe	Gly	Gln	Ala	Gly	Ile	His
				85						90					95	
	Cys	Pro	Met	Ala	Thr	Asp	Ala	Ser	Ala	Thr	Glu	Phe	Asp	Arg	Ser	Ala
5				100					105					110		
	Glu	Cys	Ala	Glu	Arg	Thr	Ser	Ala	Gln	Ile	Asp	Thr	Ala	Ile	Arg	Ser
				115					120					125		
	Gln	Ser	Gln	Ile	Ile	Arg	Thr	His	Ile	Asp	Thr	Cys	Pro	Lys	Ser	Ser
				130					135					140		
10	Gly	Thr	Ile	Gly	Gly	Ser	Thr	His	Thr	Ser	Leu	His	Leu	Lys	Val	Phe
	145								150					155		160
	Asp	Gly	Arg	Gly	Glu	Val	Gly	His	Ile	His	Pro	Lys	Asp	Gly	Leu	Arg
									165					170		175
	Phe	Gly	Val	Val	Glu	Gly	Tyr	Ser	Ile	Gly	Ser	Tyr	Val	Asp	Ala	Ile
15				180					185					190		
	Gly	Ile	Gly	Ala	Thr	His	Ala	Lys	Ala	Gly	Ile	Ser	Asp	Thr	Arg	Thr
				195					200					205		
	Gly	Ile	Ala	Gly	Gly	Tyr	His	Gly	Gly	Ser	Gln	His	Gln	Gln	Ile	Gly
				210					215					220		
20	Asp	Val	Thr	Thr	Ile	Ile	Gly	Leu	Gly	Lys	Phe	Gly	Leu	Ala	Asn	Val
	225								230					235		240
	Gly	Val	Ser	Asp	Arg	Gly	Phe	Arg	Arg	Gly	Ala	Ser	Ser	Tyr	Asp	Leu
									245					250		255
	Tyr	Gly	Leu	Glu	Leu	His	Ile	Ala	Lys	Thr	Ile	Tyr	Leu	Ala	Val	Gly
25				260					265					270		
	Asp	Gly	Cys	Leu	Cys	Arg	Gln	Ala	Glu	Arg	Gln	Asp	Gly			
				275					280					285		

(2) INFORMATION FOR SEQ ID NO:98

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...240

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

```

Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu Gly Leu Cys
1           5           10           15
15 Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly His Ser Ile
           20           25           30
Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr Val Glu Asn
           35           40           45
Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile Asp Met Asp
20           50           55           60
Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile Ser Arg Glu
65           70           75           80
Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu Tyr Asn Gly
           85           90           95
25 Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu Ile Gly Ala
           100          105          110
Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe Thr Ile Thr
           115          120          125
Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr Tyr Gln Ile
30           130          135          140
Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu Thr Phe Asn
145          150          155          160
Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro Ile Gly Gly
           165          170          175
35 Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser Glu Pro Gln
           180          185          190

```

Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys Asp Phe Asn
 195 200 205
 Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe Ala Arg Met
 210 215 220
 5 Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp Thr Phe Asn
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:99

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- 20 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...399
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala
 1 5 10 15
 30 Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu
 20 25 30
 Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile Arg Ser Ala
 35 40 45
 Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val Lys Gly Tyr
 35 50 55 60
 Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr Ser Leu Pro

	65		70		75		80									
	Ala	Ala	His	Gly	Val	Lys	Leu	Ser	Leu	Gly	Val	Ser	Thr	Leu	Asn	Tyr
				85					90						95	
	Trp	Gly	Ala	Ser	Arg	Tyr	Pro	Ala	Gly	Ile	Ala	Tyr	Ser	Asp	Leu	Pro
5			100						105					110		
	Tyr	Trp	Thr	Asp	Tyr	Asn	Asp	Tyr	Val	Arg	Leu	Arg	Ile	Leu	Pro	Tyr
			115						120					125		
	Val	Gln	Ala	Met	Leu	Lys	Pro	Thr	Ala	Thr	Thr	Ala	Leu	Met	Leu	Gly
			130						135					140		
10	Asn	Ile	Ala	Gly	Gly	Thr	Ala	His	Gly	Leu	Ile	Glu	Pro	Ile	Tyr	Asn
			145						150					155		160
	Pro	Glu	Leu	Asp	Leu	Thr	Ala	Asp	Pro	Glu	Ala	Gly	Val	Gln	Phe	Arg
									165					170		175
	Gly	Asp	Trp	Thr	Arg	Phe	Arg	Met	Asp	Val	Trp	Val	Asn	Trp	Met	Ser
15			180						185					190		
	Met	Ile	Phe	Lys	Asn	Asp	Asn	His	Gln	Glu	Ser	Phe	Val	Phe	Gly	Leu
			195						200					205		
	Ser	Thr	Thr	Ser	Lys	Leu	Leu	Ser	Gly	Glu	Gly	Lys	Trp	Arg	Leu	Glu
			210						215					220		
20	Leu	Pro	Leu	Gln	Ala	Ile	Ala	Thr	His	Arg	Gly	Gly	Glu	Tyr	Asn	Trp
			225						230					235		240
	Ala	Gln	Gln	Asp	Thr	Val	His	Thr	Trp	Val	Asn	Gly	Ala	Val	Gly	Leu
									245					250		255
	Lys	Leu	Ser	Tyr	Arg	Pro	Arg	Thr	Asp	Lys	Pro	Met	Gln	Ile	Trp	Gly
25			260						265					270		
	Ser	Ala	Tyr	Gly	Val	Ala	Ala	Leu	Ser	Ser	Gly	Gly	Tyr	Phe	Pro	Tyr
			275						280					285		
	Glu	Arg	Gly	Trp	Gly	Gly	Tyr	Leu	Ser	Leu	Gly	Met	Asp	Leu	Glu	His
			290						295					300		
30	Phe	Ala	Phe	Arg	Thr	Asp	Tyr	Trp	Tyr	Gly	Arg	His	Tyr	Val	Ser	Pro
			305						310					315		320
	Phe	Ala	Ala	Pro	Phe	Ala	Asn	Ser	Leu	Thr	Tyr	Asp	Lys	Gln	Pro	Leu
									325					330		335
	Thr	Asn	Gly	Trp	Gly	Asp	Tyr	Ile	Arg	Leu	Tyr	Ala	Asp	Tyr	Ser	Trp
35			340						345					350		
	Arg	Met	Ala	Arg	Ser	Val	Ser	Leu	Ala	Ala	Val	Ala	Arg	Val	Trp	Phe

```

          355          360          365
Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu Leu Thr Met
      370          375          380
Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly Asn His
5  385          390          395

```

(2) INFORMATION FOR SEQ ID NO:100

```

      (i) SEQUENCE CHARACTERISTICS:
10      (A) LENGTH: 382 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein
15

      (iii) HYPOTHETICAL: YES

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Porphyromonas gingivalis
20

      (ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...382

25      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

```

```

Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly Met
1          5          10          15
Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu Pro
30          20          25          30
Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys Leu
          35          40          45
Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val Asp
          50          55          60
35 Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser
65          70          75          80

```


	Ala	His	Gly	Glu	Leu	Asn	Arg	His	Leu	Ser	Phe	Asp	Trp	Arg	Gln	Arg	
					85					90					95		
	Leu	Asn	Arg	Ala	Ala	Asp	Gly	Thr	Ser	Phe	Ala	Asp	Asn	Leu	Ser	Asn	
				100					105					110			
5	Ala	Ile	Asp	Ile	Ala	Gly	Val	Asp	Trp	His	Pro	Asn	Asp	Lys	Val	Ser	
			115				120						125				
	Phe	Phe	Phe	Gly	Arg	Gln	Tyr	Ala	Arg	Phe	Gly	Gly	Ile	Glu	Tyr	Asp	
			130				135					140					
	Met	Asn	Pro	Val	Glu	Ile	Tyr	Gln	Tyr	Ser	Asp	Leu	Val	Asp	Tyr	Met	
10	145					150				155					160		
	Thr	Cys	Tyr	Thr	Ser	Gly	Val	Asn	Phe	Ala	Trp	Asn	Phe	His	Pro	Glu	
					165					170				175			
	Gln	Gln	Leu	Gln	Leu	Gln	Val	Leu	Asn	Ala	Tyr	Asn	Asn	Arg	Phe	Ala	
				180					185					190			
15	Asp	Arg	Tyr	His	Val	Thr	Pro	Asp	Val	Ala	Thr	Ala	Thr	Ser	Tyr	Pro	
			195				200						205				
	Leu	Leu	Tyr	Ser	Ala	Gln	Trp	Asn	Gly	Thr	Leu	Leu	Gly	Gly	Ala	Leu	
			210				215						220				
	His	Met	Arg	Tyr	Ala	Val	Ser	Met	Ala	His	Gln	Ala	Gln	Glu	Arg	Asn	
20	225					230				235					240		
	Met	Trp	Tyr	Phe	Thr	Ala	Gly	Asn	Leu	Phe	Asn	Pro	Gly	Lys	Arg	Ile	
				245						250				255			
	Asn	Gly	Tyr	Leu	Asp	Leu	Thr	Tyr	Ser	Ile	Glu	Gly	Leu	Asp	Asp	Lys	
			260						265				270				
25	Gly	Ile	Met	Thr	Ala	Arg	Tyr	Gly	Lys	Gly	Lys	Thr	Leu	Thr	Asp	Val	
			275					280					285				
	Lys	Tyr	Tyr	Ala	Leu	Val	Ser	Lys	Trp	Asn	Phe	Arg	Ile	Phe	Asp	Gln	
			290					295				300					
	Val	Asn	Leu	Phe	Leu	Lys	Gly	Met	Tyr	Glu	Asn	Gly	Tyr	Ala	Pro	Ala	
30	305					310				315					320		
	Gln	Tyr	Gly	Glu	Ser	Ser	His	Thr	Arg	His	Ser	Tyr	Gly	Tyr	Met	Gly	
				325						330				335			
	Gly	Val	Glu	Tyr	Tyr	Pro	Thr	Glu	Thr	Asn	Phe	Arg	Leu	Phe	Val	Thr	
				340						345				350			
35	Tyr	Ile	Gly	Arg	His	Tyr	Arg	Tyr	Ser	Ala	Thr	Glu	Thr	Glu	Ser	Thr	
			355							360				365			

Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:101

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...494

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Tyr Ile Leu Ser Ser
 25 1 5 10 15
 Ile Ser Leu Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu
 20 25 30
 Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile
 35 40 45
 30 Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe
 50 55 60
 Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser
 65 70 75 80
 Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn
 35 85 90 95
 Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg

	100	105	110
	Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Phe Gly		
	115	120	125
	Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Pro Ser Ile Asn		
5	130	135	140
	Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly		
	145	150	155
	His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu		
	165	170	175
10	Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe		
	180	185	190
	Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser		
	195	200	205
	Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly		
15	210	215	220
	Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala		
	225	230	235
	Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu		
	245	250	255
20	Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe		
	260	265	270
	Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu		
	275	280	285
	Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly		
25	290	295	300
	Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys		
	305	310	315
	Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala		
	325	330	335
30	Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg		
	340	345	350
	Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met		
	355	360	365
	Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn		
35	370	375	380
	Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn		

```

385          390          395          400
Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr
          405          410          415
Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser
5          420          425          430
Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser
          435          440          445
Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala
          450          455          460
10 Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser
465          470          475          480
Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe
          485          490

```

15 (2) INFORMATION FOR SEQ ID NO:102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
 (B) TYPE: amino acid
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- 30 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

```

35 Met Lys Arg Leu Ile Val Phe Leu Ala Met Gly Gly Leu Leu Phe Thr
1          5          10          15

```

Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala Ser Asp Thr Pro Lys Lys
 20 25 30
 Asp Trp Thr Ile Lys Gly Val Thr Gly Leu Asn Ala Ser Gln Thr Ser
 35 40 45
 5 Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn Thr Val Ala Gly Asn Leu
 50 55 60
 Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys Asp Lys Trp Ser Trp Asp
 65 70 75 80
 Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr Tyr Thr Thr Ala Asn Lys
 85 90 95
 10 Trp Asn Lys Ser Val Asp Lys Ile Glu Leu Phe Thr Lys Ala Gly Tyr
 100 105 110
 Glu Ile Gly Lys His Trp Tyr Gly Ser Ala Leu Phe Thr Phe Leu Ser
 115 120 125
 15 Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser Asp His Leu Thr Gly Val
 130 135 140
 Lys His Ile Ser Asn Phe Phe Ala Pro Ala Tyr Leu Thr Leu Gly Ile
 145 150 155 160
 Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe Ser Leu Tyr Leu Ser Pro
 165 170 175
 20 Thr Thr Gly Lys Leu Thr Val Val Ala Asp Asp Tyr Leu Ser Ser Leu
 180 185 190
 Gly Ala Phe Gly Val Lys Val Gly Glu Lys Thr Met Phe Glu Leu Gly
 195 200 205
 25 Ala Leu Val Val Gly Ser Ala Asn Ile Asn Leu Met Glu Asn Val Asn
 210 215 220
 Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala Tyr Thr His Asp Phe Gly
 225 230 235 240
 Asn Ile Asp Ile Asn Trp Glu Ala Met Leu Ala Met Lys Ile Asn Lys
 245 250 255
 30 Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu Ile Tyr Asp Asp Asp Val
 260 265 270
 Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe Lys Glu Val Val Gly Val
 275 280 285
 35 Gly Val Ala Tyr Thr Phe
 290

(2) INFORMATION FOR SEQ ID NO:103

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 961 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

15

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...961

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

Met	Lys	Lys	Leu	Phe	Pro	Leu	Leu	Leu	Leu	Ile	Leu	Ser	Ile	Leu	Val
1				5						10				15	
Gly	Cys	Gly	Lys	Lys	Glu	Lys	His	Ser	Val	Thr	Glu	Ile	Ala	Unk	Glu
25				20				25						30	
Lys	Lys	Arg	Ile	Thr	Ala	Leu	Leu	Tyr	Glu	Lys	Glu	Leu	Pro	Thr	Asp
				35				40						45	
Ser	Val	Lys	Gln	Leu	Tyr	Glu	Asn	Ser	Val	Gln	Asn	Lys	Asn	Leu	Val
				50				55						60	
30	Gly	Gln	Met	Leu	Phe	Ala	Ile	Glu	Val	Gly	Lys	Arg	Met	Arg	Asn
				65				70						75	
Ser	Gln	Tyr	Thr	Asp	Ala	Met	Leu	Tyr	His	Gln	Lys	Gly	Leu	Asn	Ala
				85				90						95	
Ala	Leu	Asn	Leu	Arg	Asp	Thr	Ile	Val	Ala	Ala	Gln	Ala	Trp	Asn	His
35				100				105						110	
Leu	Gly	Thr	Asp	Ser	Arg	Arg	Ile	Gly	Ala	Leu	Ala	Glu	Ala	Ser	Asp

	115		120		125	
	Tyr His Tyr Lys Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln					
	130		135		140	
	Asn Arg Pro Ala Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly					
5	145		150		155	160
	Asn Ile Asn Leu Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe					
		165		170		175
	Leu Lys Ala Leu Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln					
		180		185		190
10	Ala Ile Asn Tyr Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu					
		195		200		205
	Tyr Asp Lys Ala Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn					
		210		215		220
	Met Ala Glu Asn Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly					
15	225		230		235	240
	Glu Val Asp Glu Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr					
		245		250		255
	Ala Thr Ala Tyr Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp					
		260		265		270
20	Leu Asn Ser Cys Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn					
		275		280		285
	Glu Arg Leu Tyr Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys					
		290		295		300
	Glu Ile Asn Ser Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr					
25	305		310		315	320
	Glu Asn Leu Glu Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe					
		325		330		335
	Cys Leu Ser Lys Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val					
		340		345		350
30	Ser Ser Ile Gln Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln					
		355		360		365
	Lys Glu Leu Glu Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys					
		370		375		380
	Ser Lys Phe Ile Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile					
35	385		390		395	400
	Leu Leu Ile Ser Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His					

		405		410		415										
	Asn	Lys	Leu	Ile	Lys	Glu	Thr	Asp	Lys	Leu	Arg	Ser	Gly	Phe	Phe	Thr
		420		425		430										
	Gly	Ile	Thr	His	Glu	Phe	Arg	Thr	Pro	Ile	Thr	Val	Ile	Gln	Gly	Leu
5		435		440		445										
	Asn	Glu	Lys	Met	Ser	Ser	Ser	Pro	Asp	Leu	Gln	Ala	Ser	Asp	Arg	Thr
		450		455		460										
	Glu	Leu	His	Lys	Ile	Ile	Asp	Arg	Gln	Ser	Ser	His	Met	Leu	Asn	Leu
	465			470		475									480	
10	Val	Asn	Gln	Leu	Leu	Asp	Ile	Cys	Lys	Ile	Arg	Ser	Gly	Val	Ser	Thr
		485		490		495										
	Pro	Glu	Trp	Arg	Asn	Gly	Asp	Ile	Val	Ser	Phe	Val	Gln	Ile	Leu	Ile
		500		505		510										
	Asp	Ser	Phe	Ala	Pro	Tyr	Ala	Gln	Ala	Gln	Asp	Ile	Thr	Leu	Glu	Leu
15		515		520		525										
	Gln	Pro	Glu	Ser	Lys	Pro	Ile	Val	Val	Asp	Phe	Val	Pro	Ser	Tyr	Leu
		530		535		540										
	Gln	Lys	Ile	Ile	Ser	Asn	Leu	Leu	Ser	Asn	Ala	Ile	Lys	Tyr	Ser	Leu
	545			550		555									560	
20	Ala	Gly	Gly	Arg	Val	Val	Ile	Ser	Leu	Ala	Lys	Thr	Lys	Asn	Glu	Lys
		565		570		575										
	Asn	Leu	Ile	Ile	Arg	Val	Ala	Asp	Asn	Gly	Ile	Gly	Ile	Asp	Lys	Thr
		580		585		590										
	Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
25		595		600		605										
	Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		610		615		620										
	Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
	625			630		635									640	
30	Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		645		650		655										
	Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		660		665		670										
	His	Ile	Ala	Pro	Asp	Asp	Ser	Pro	Thr	Ser	Pro	Met	Val	Ala	Ala	Leu
35		675		680		685										
	Asn	His	Arg	Phe	Glu	Asp	Glu	Arg	Pro	Thr	Ile	Leu	Leu	Val	Glu	Asp

	690		695		700	
	Asn Lys Asp Ile Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr					
	705		710		715	720
	Asn Val Leu Ser Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr					
5		725		730		735
	Glu His Ile Pro Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met					
		740		745		750
	Asp Gly Ile Glu Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys					
		755		760		765
10	His Ile Pro Ile Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg					
		770		775		780
	Leu Glu Gly Ile Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe					
		785		790		795
	Ser Pro Glu Glu Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg					
15		805		810		815
	Glu Leu Leu Lys Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys					
		820		825		830
	Pro Glu Glu Glu Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu					
		835		840		845
20	Leu Ala Ala Lys Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp					
		850		855		860
	Phe Ser Ala Gln Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln					
		865		870		875
	Leu Asn Arg Lys Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr					
25		885		890		895
	Ile Gln Gln Ile Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu					
		900		905		910
	Ser Lys Asn Ile Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro					
		915		920		925
30	Ala Tyr Phe Ser Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser					
		930		935		940
	Gln Tyr Arg Gln Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr					
		945		950		955
	Val					960

(2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 222 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

20
 Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser
 1 5 10 15
 Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn Asn Thr Glu Lys Ser
 20 25 30-
 25 Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser
 35 40 45
 Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu
 50 55 60
 Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala
 30 65 70 75 80
 Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val
 85 90 95
 Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val
 100 105 110
 35 Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe
 115 120 125

```

Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His
 130                      135                      140
Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys
145                      150                      155                      160
5 Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His
                      165                      170                      175
Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr Asp Leu Thr Ser Cys
                      180                      185                      190
Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe
10                      195                      200                      205
Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu
                      210                      215                      220

```

(2) INFORMATION FOR SEQ ID NO:105

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1158 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

30

(B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

```

Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala
35 1                      5                      10                      15
Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp

```

	20	25	30
	Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala		
	35	40	45
	Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe		
5	50	55	60
	Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Gly Val Leu		
	65	70	75 80
	Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro		
	85	90	95
10	Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val		
	100	105	110
	Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn		
	115	120	125
	Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala		
15	130	135	140
	Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala		
	145	150	155 160
	Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr		
	165	170	175
20	Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala		
	180	185	190
	Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser		
	195	200	205
	Ser Gly Glu Leu Gly Thr Val Phe Ser Tyr Ile Ala Lys Ala Arg Ser		
25	210	215	220
	Ala Gly Gly Gly Arg Glu Met Ser Leu Ser Ala Asn Gly Ile Leu Ile		
	225	230	235 240
	Phe Ser Asp Pro Phe Ser Met Thr Ser Asn Glu Val Ser Asn Ser Tyr		
	245	250	255
30	Leu Ala Gly Lys Lys Arg Arg Leu Tyr His Ser Thr Pro Met Asn Ser		
	260	265	270
	Leu Val Asn Glu Leu Arg Leu Asp Ala Asn Tyr Ser Met Thr Gly Asp		
	275	280	285
	Ala Val Asn Leu Asp Phe Ile Glu Val Ala Thr Gln Asn Asp Leu Arg		
35	290	295	300
	Tyr Asp Gly Ala Pro Met His Ile Arg Arg Phe Ser Asn Leu Pro Val		

	305		310		315		320
	Leu Gly Gly Glu Ser Cys Arg Phe Val Ile Ser Glu Val Pro Glu Ser						
		325		330		335	
	Leu Val Val Leu Gln Ala Asn Ser Ser Leu Thr Ala Ser Leu Val Pro						
5		340		345		350	
	Val Lys Thr Val Gly Asp Lys Thr Ile Glu Phe Val Ala Pro Pro Lys						
		355		360		365	
	Gly Gln Asp Arg Arg Thr Ile Asn Thr Phe Tyr Ala Val Asp Leu Ser						
		370		375		380	
10	Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro Asn Gln Asn Leu						
		385		390		395	400
	His Gly Glu Glu Ile Pro Asp Leu Ile Ile Val Ser Thr Gln Ala Leu						
		405		410		415	
	Leu Leu Glu Ala Asp Arg Leu Ala Thr Tyr Arg Arg Glu Lys Asn Gly						
15		420		425		430	
	Leu Lys Val Leu Val Val Leu Gln Glu Gln Val Phe Asn Glu Phe Ser						
		435		440		445	
	Gly Gly Thr Pro Asp Ala Thr Ala Tyr Arg Leu Phe Ala Lys Met Phe						
		450		455		460	
20	Tyr Asp Arg Trp Lys Ala Asn Ala Pro Val Gly Glu Thr Phe Pro Met						
		465		470		475	480
	Gln Met Leu Leu Phe Gly Asp Gly Ala His Asp Asn Arg Lys Val Ser						
		485		490		495	
	Val Ala Trp Gln Lys Pro Tyr Leu Gln Gln Thr Glu Phe Leu Leu Thr						
25		500		505		510	
	Phe Gln Ala Val Asn Ser Thr Asn Val Asn Ser Tyr Val Thr Asp Asp						
		515		520		525	
	Tyr Phe Gly Leu Leu Asp Asp Gln Pro Ala Ser Val Asn Ile Gly Trp						
		530		535		540	
30	Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val Arg Thr Pro Ala						
		545		550		555	560
	Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr Glu Glu Asp Arg						
		565		570		575	
	Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala Ala Asp Asn Gly						
35		580		585		590	
	Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp Thr Val Lys Arg						

	595	600	605
	Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln Asp Val Tyr Pro		
	610	615	620
	His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly Ala Lys Lys Lys		
5	625	630	635 640
	Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu Asn Tyr Ala Gly		
	645	650	655
	His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu Leu Thr Leu Asn		
	660	665	670
10	Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile Trp Ile Thr Ala		
	675	680	685
	Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr Ser Ala Gly Glu		
	690	695	700
	Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile Met Phe Ser Thr		
15	705	710	715 720
	Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile Asn Gly Phe Met		
	725	730	735
	Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg Tyr Arg Thr Met		
	740	745	750
20	Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu Ser Thr Val Phe		
	755	760	765
	Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met Gly Asp Pro Ser		
	770	775	780
	Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu Thr Ala Ile Asn		
25	785	790	795 800
	Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met Leu Lys Ser Leu		
	805	810	815
	Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu Lys Gly Thr Phe		
	820	825	830
30	Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val Phe Asp Gly Arg		
	835	840	845
	Lys Lys Met Thr Ala Leu Glu Glu Gly Asn Asp Leu Ser Leu Val		
	850	855	860
	Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile Ala Glu Val Lys		
35	865	870	875 880
	Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys Asp Val Asn Tyr		

	885	890	895
	Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr Asn Glu Ser Thr		
	900	905	910
	Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg Val Gln Pro Gly		
5	915	920	925
	Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro Glu Ile Ile Ser		
	930	935	940
	Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp Glu Val Asn Pro		
	945	950	955
10	Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn Gly Ile Asn Ile		
	965	970	975
	Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys Ile Asp Gly Arg		
	980	985	990
	Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr Ser Ser Ala Thr		
15	995	1000	1005
	Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro Ala Leu Ala Glu		
	1010	1015	1020
	Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile Phe Asn Asn Ala		
	1025	1030	1035
20	Val His His Asp Phe Ser Phe Arg Val Val Asp Gly Ile Ala Pro Asp		1040
	1045	1050	1055
	Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg Glu Ser Ala Thr		
	1060	1065	1070
	Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu Asn Val Ala Val		
25	1075	1080	1085
	Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser Leu Pro Val Lys		
	1090	1095	1100
	Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile Lys Trp Asp Leu		
	1105	1110	1115
30	Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe Tyr Leu Tyr Arg		1120
	1125	1130	1135
	Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser Met Ala Lys Lys		
	1140	1145	1150
	Met Ile Val Val Gly Gln		
35	1155		

(2) INFORMATION FOR SEQ ID NO:106

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

20

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Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile
1           5           10           15
Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn
          20           25           30
25 Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg
          35           40           45
Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr
          50           55           60
Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala
30 65           70           75           80
Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp
          85           90           95
Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu
          100          105          110
35 Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu
          115          120          125

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Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn
 130 135 140
 Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe
 145 150 155 160
 5 Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His
 165 170 175
 Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala
 180 185 190
 Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp
 10 195 200 205
 Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp
 210 215 220
 Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr
 225 230 235 240
 15 Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu
 245 250 255
 Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn
 260 265 270
 Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser
 20 275 280 285
 Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu
 290 295 300
 Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser
 305 310 315 320
 25 Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro
 325 330 335
 Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met
 340 345 350
 Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser
 30 355 360 365
 Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp
 370 375 380
 Gly Leu Arg Asn Leu Phe His
 385 390
 35

(2) INFORMATION FOR SEQ ID NO:107

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

15 (A) NAME/KEY: misc_feature

(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

20 Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly
 1 5 10 15
 Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe
 20 25 30
 Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn
 25 35 40 45
 Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala Leu
 50 55 60
 Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg
 65 70 75 80
 30 Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr
 85 90 95
 Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn
 100 105 110
 Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala
 35 115 120 125
 Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala

130 135 140
 Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser
 145 150 155 160
 Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His
 5 165 170 175
 Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg
 180 185 190
 Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
 195 200

10

(2) INFORMATION FOR SEQ ID NO:108

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 455 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

25 (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

30

Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu
 1 5 10 15
 Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met
 20 25 30
 35 Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn
 35 40 45

Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser
 50 55 60
 Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile
 65 70 75 80
 5 Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr
 85 90 95
 Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val
 100 105 110
 Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys
 10 115 120 125
 Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp
 130 135 140
 Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln
 145 150 155 160
 15 Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln
 165 170 175
 Arg Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly
 180 185 190
 Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu
 20 195 200 205
 Val Gln Tyr Arg Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln
 210 215 220
 Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp
 225 230 235 240
 25 Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu
 245 250 255
 Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser
 260 265 270
 Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala
 30 275 280 285
 Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr
 290 295 300
 Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser
 305 310 315 320
 35 Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn
 325 330 335

Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser
 340 345 350
 Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys
 355 360 365
 5 Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala
 370 375 380
 Asp Lys Ala Ile Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys
 385 390 395 400
 Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala
 10 405 410 415
 Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu
 420 425 430
 Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp
 435 440 445
 15 Phe Tyr Gln Gly Lys Asp Phe
 450 455

(2) INFORMATION FOR SEQ ID NO:109

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- 30 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...434
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

	Met	Tyr	Lys	Asp	Tyr	Lys	Gly	Leu	Tyr	Ala	Ser	Leu	Arg	Trp	Tyr	Ala
	1				5					10					15	
	Leu	Ile	Ile	Gly	Leu	Leu	Phe	Ala	Ala	Asp	Gly	Ile	Gln	Ala	Gln	Asn
5				20					25					30		
	Asn	Asn	Phe	Thr	Glu	Ser	Pro	Tyr	Thr	Arg	Phe	Gly	Leu	Gly	Arg	Leu
			35					40					45			
	Gly	Glu	Arg	Thr	Thr	Ile	Ser	Gly	His	Ser	Met	Gly	Gly	Leu	Gly	Val
		50					55					60				
10	Gly	Leu	Arg	Gln	Gly	Thr	Tyr	Val	Asn	Ala	Val	Asn	Pro	Ala	Ser	Tyr
	65					70					75				80	
	Ser	Ala	Val	Asp	Ser	Met	Thr	Phe	Ile	Phe	Asp	Phe	Gly	Ala	Ser	Thr
				85					90					95		
	Gly	Ile	Thr	Trp	Tyr	Ala	Glu	Asn	Gly	Lys	Lys	Asp	Asn	Arg	Lys	Met
15				100				105						110		
	Gly	Asn	Ile	Glu	Tyr	Phe	Ala	Met	Leu	Phe	Pro	Ile	Ser	Lys	Ser	Ile
		115						120					125			
	Ala	Met	Ser	Ala	Gly	Val	Leu	Pro	Tyr	Ser	Ala	Ser	Gly	Tyr	Gln	Phe
		130					135						140			
20	Gly	Ser	Val	Asp	Gln	Val	Glu	Gly	Gly	Ser	Val	Gln	Tyr	Thr	Arg	Lys
	145					150					155				160	
	Tyr	Leu	Gly	Thr	Gly	Asn	Leu	Asn	Asp	Leu	Tyr	Val	Gly	Ile	Gly	Ala
				165					170					175		
	Thr	Pro	Phe	Lys	Asn	Phe	Ser	Ile	Gly	Ala	Asn	Ala	Ser	Ser	Leu	Phe
25				180					185					190		
	Gly	Arg	Phe	Thr	His	Ser	Arg	Gln	Val	Ile	Phe	Ser	Thr	Glu	Ala	Pro
		195						200					205			
	Tyr	Asn	Pro	Val	His	Leu	Ser	Thr	Leu	Tyr	Leu	Lys	Ala	Ala	Lys	Phe
		210					215					220				
30	Asp	Phe	Gly	Met	Gln	Tyr	His	Leu	Leu	Leu	Lys	Ser	Asp	Arg	Ser	Leu
	225					230					235				240	
	Val	Ile	Gly	Ala	Val	Tyr	Ser	Pro	Arg	Val	Lys	Met	His	Ser	Glu	Leu
				245					250					255		
	Thr	Gln	Ile	Lys	Asn	Gln	Val	Gln	Asn	Gly	Val	Val	Val	Glu	Ser	Glu
35				260					265					270		
	Thr	Gln	Glu	Tyr	Ile	Lys	Gly	Met	Asp	Tyr	Tyr	Thr	Leu	Pro	His	Thr

	275	280	285
	Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu Leu Gly		
	290	295	300
	Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr Lys Ser		
5	305	310	315 320
	Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly Glu Ile		
	325	330	335
	Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg Tyr Arg		
	340	345	350
10	Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr Lys Gly		
	355	360	365
	Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly Ile Gly		
	370	375	380
	Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu Glu Tyr		
15	385	390	395 400
	Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala Leu Lys		
	405	410	415
	Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys Leu Lys		
	420	425	430
20	Leu Asn		

(2) INFORMATION FOR SEQ ID NO:110

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 926 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- 35 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...926

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

```

Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu Ala Ser Leu
1           5           10           15
Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala Gly Arg Val
10          20          25          30
Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val Gln Leu Val
          35          40          45
Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr Asn Glu Lys
          50          55          60
15 Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr Ile Leu Arg
65          70          75          80
Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile Ser Leu Arg
          85          90          95
Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn Glu Asp Ala
20          100         105         110
Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala Glu Val Val
          115         120         125
Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr Thr Val Ala
          130         135         140
25 Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro Gly Ala Glu
145          150          155          160
Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp Ile Ser Lys
          165          170          175
Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro Gln Val Ala
30          180         185         190
Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln Val Leu Asn
          195         200         205
Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp Gly Glu Glu
          210         215         220
35 Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys Lys Gly Leu
225          230          235          240

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Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg Tyr Met Ala
 245 250 255
 Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp Thr Leu Ile
 260 265 270
 5 Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu Met Asp Ser
 275 280 285
 Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly Gly Arg Arg
 290 295 300
 Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met Leu Gly Gly
 10 305 310 315 320
 Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly Gly Asp Ala
 325 330 335
 Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys Arg Val Glu
 340 345 350
 15 Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn Ile Leu Glu
 355 360 365
 Arg Ser Phe Ser His Asn Gly Gln Ala Arg Phe Arg Met Gln Trp Lys
 370 375 380
 Pro Ser Glu Arg Thr Glu Val Val Phe Glu Pro Asp Leu Ser Ile Ser
 20 385 390 395 400
 Lys Ile Asp Gly Phe Phe Asn Asp Thr Tyr Glu Thr Lys Asp Ala Thr
 405 410 415
 Gly Ile Ser Ile Asn Lys Gly Ser Ile His Gln Thr Thr Gln Gly Asn
 420 425 430
 25 Asn Phe Arg Leu Asn Gly Glu Leu Asp Ile Ser His Lys Leu Asn Asp
 435 440 445
 Glu Gly Arg Thr Ile Ser Ala Ser Val Ser Gly Gly Leu Thr Asp Glu
 450 455 460
 Asp Gly Asp Gly Ile Tyr Gln Ala Val Leu Gln Ser Val Glu Thr Asn
 30 465 470 475 480
 Gln Lys Gln Phe Asn Asp Asn Ser Asn Leu Gln Tyr Arg Leu Arg Leu
 485 490 495
 Ser Tyr Val Glu Pro Leu Gly Lys Asn Tyr Phe Ala Gln Ala Ile Leu
 500 505 510
 35 Asn Arg Arg Phe Ser Arg Arg Asn Ser Asp Arg Glu Val Tyr Arg Leu
 515 520 525

Gly Asp Asp Gly Gln Tyr Ser Ile Leu Asp Ser Gln Tyr Gly Leu Ser
 530 535 540
 Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn Leu Lys Lys
 545 550 555 560
 5 Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val Asp Pro Asn
 565 570 575
 Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln Asp Lys Leu
 580 585 590
 Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile Asn Tyr Lys
 10 595 600 605
 Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly Arg Thr Thr
 610 615 620
 Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile Thr Asn Pro
 625 630 635 640
 15 Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser Tyr Ser Asn
 645 650 655
 Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser Gln Arg Ala
 660 665 670
 Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp Ile Val Pro
 20 675 680 685
 Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr Arg Tyr Glu
 690 695 700
 Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr Leu Ser Leu
 705 710 715 720
 25 Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu Phe Asn Arg
 725 730 735
 Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn Lys Ala Leu
 740 745 750
 Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg Asn Asn Trp
 30 755 760 765
 Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met Ala Asn Asn
 770 775 780
 Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe Gly Gly Asn
 785 790 795 800
 35 Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile Asp Ser Asp
 805 810 815

Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe Ser Leu Asp
 820 825 830
 Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu Arg Asp Lys
 835 840 845
 5 Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly Gln Arg Ser
 850 855 860
 Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu Ser Met Ser
 865 870 875 880
 Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr Arg Phe Asn
 10 885 890 895
 Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg Gly Asn Met
 900 905 910
 Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro Ser
 915 920 925
 15

(2) INFORMATION FOR SEQ ID NO:111

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 781 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

30 (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

35

Met Asp Arg Pro Lys Pro Ser Tyr Ile Val Arg Ile Ala Ala Ile Leu

	1				5					10					15				
	Cys	Leu	Phe	Val	Gly	Arg	Pro	Leu	Phe	Ala	Gln	Ser	Tyr	Val	Asp	Tyr			
				20					25					30					
	Val	Asp	Pro	Leu	Ile	Gly	Thr	Leu	Ser	Ser	Phe	Glu	Leu	Ser	Ala	Gly			
5			35					40					45						
	Asn	Thr	Tyr	Pro	Val	Ile	Gly	Leu	Pro	Trp	Gly	Met	Asn	Ser	Trp	Thr			
		50					55					60							
	Pro	Met	Thr	Gly	Val	Pro	Gly	Asp	Gly	Trp	Gln	Tyr	Thr	Tyr	Ser	Ala			
	65					70					75					80			
10	His	Lys	Ile	Arg	Gly	Phe	Lys	Gln	Thr	His	Gln	Pro	Ser	Pro	Trp	Ile			
				85						90					95				
	Asn	Asp	Tyr	Gly	Gln	Phe	Ser	Leu	Leu	Pro	Leu	Thr	Ala	Pro	Gln	Lys			
			100						105				110						
	Pro	Ser	Ser	Asn	Asp	Ser	Ile	Ala	Leu	Thr	Lys	Trp	Cys	Lys	Gln	Leu			
15			115					120					125						
	Phe	Ser	Asp	Glu	Gln	Thr	Ser	Trp	Phe	Ser	His	Lys	Ala	Glu	Thr	Ala			
		130					135					140							
	Thr	Pro	Tyr	Tyr	Tyr	Ser	Val	Tyr	Leu	Ala	Asp	Tyr	Asp	Thr	Arg	Val			
	145					150					155					160			
20	Glu	Met	Ala	Pro	Thr	Glu	Arg	Ala	Ala	Ile	Phe	Arg	Ile	Arg	Tyr	Ser			
				165						170					175				
	Gly	Asn	Thr	Glu	Ser	Gly	Ser	Gly	Arg	Trp	Leu	Arg	Leu	Asp	Ala	Phe			
			180						185				190						
	Thr	Gly	Gly	Ser	Glu	Ile	Ser	Ile	Val	Asp	Pro	His	Thr	Val	Val	Gly			
25			195					200					205						
	Ile	Ser	Arg	Lys	Asn	Ser	Gly	Gly	Val	Pro	Ala	Asn	Phe	Ala	Cys	Tyr			
		210					215					220							
	Phe	Ile	Leu	Gln	Ser	Asp	Thr	Pro	Met	Ala	Asp	Val	Leu	Leu	Glu	Thr			
	225					230				235					240				
30	Asp	Thr	Gly	Lys	Ser	Asp	Glu	Gly	Thr	Arg	Ala	Trp	Ala	Ala	Cys	Arg			
				245						250					255				
	Phe	Asp	Ser	Gln	Glu	Val	Thr	Val	Arg	Val	Ala	Ser	Ser	Phe	Ile	Ser			
			260						265				270						
	Val	Glu	Gln	Ala	Glu	Arg	Asn	Leu	Ala	Glu	Val	Lys	Gly	Gln	Ser	Phe			
35			275					280					285						
	Asp	Arg	Ile	Arg	Leu	Ala	Gly	Arg	Glu	Ala	Trp	Asn	Lys	Val	Leu	Gly			

	290		295		300	
	Arg Ile His Val Glu Gly Gly Thr Lys Asp Glu Arg Thr Thr Phe Tyr					
	305		310		315	320
	Ser Ala Leu Tyr Arg Cys Leu Leu Phe Pro Arg Arg Phe Tyr Glu Glu					
5		325		330		335
	Asp Ala Ser Gly Asn Phe Val His Tyr Ser Pro Tyr Asn Gly Glu Val					
		340		345		350
	Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg					
		355		360		365
10	Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys					
		370		375		380
	Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro					
		385		390		395
	Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser					
15		405		410		415
	Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp					
		420		425		430
	Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His					
		435		440		445
20	Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser					
		450		455		460
	Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg					
		465		470		475
	Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg					
25		485		490		495
	Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser					
		500		505		510
	Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly					
		515		520		525
30	Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp					
		530		535		540
	Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val					
		545		550		555
	Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro					
35		565		570		575
	Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp					

	580		585		590
	Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile				
	595		600		605
	Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met				
5	610		615		620
	Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg				
	625		630		635 640
	Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr				
		645		650	655
10	Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser				
	660		665		670
	Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu				
	675		680		685
	Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His				
15	690		695		700
	Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile				
	705		710		715 720
	Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr				
		725		730	735
20	His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr				
	740		745		750
	Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser				
	755		760		765
	Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn				
25	770		775		780

(2) INFORMATION FOR SEQ ID NO:112

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

10

```

Met Lys Thr Thr Val Gln Gln Ile Ile Leu Cys Leu Ala Leu Met Met
1           5           10           15
Ser Gly Val Leu Gly Gly Asn Ala Gln Ser Phe Trp Glu Glu Ile Ala
          20           25           30
15 Pro Pro Phe Ile Ser Asn Glu Pro Asn Val Lys Tyr Ile Ile Pro Asn
          35           40           45
Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr Val Thr Val Thr Lys Arg
          50           55           60
Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu Gln Leu Gly Met Tyr Tyr
20 65           70           75           80
Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp Lys His Asp Pro Tyr Phe
          85           90           95
Asp Asp Lys Ile Val Ala Asp Ile Gln Thr Asp Ala Tyr Gly Arg Val
          100          105          110
25 Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln Glu Tyr Gln Leu Tyr Ile
          115          120          125
Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe Lys Thr Ser Val Ser Thr
          130          135          140
Tyr Glu His Gly Met Ala Val Phe Arg Ser Ser Thr Gly Val Thr Tyr
30 145          150          155          160
Ile Gly Thr Arg His His Ile Phe Ala Ser Gly Val Asn Asp Phe Glu
          165          170          175
Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro Met Ser Cys Arg Phe Ala
          180          185          190
35 Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu Ala Leu Met His Glu Thr
          195          200          205

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Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln Asn Gly Glu Phe Val Asp
 210 215 220
 Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile Ile Ala Ser Met Cys Ser
 225 230 235 240
 5 Asn Lys Glu Gly Asp Ile Ile Ala Leu Val Thr Ser Tyr Thr Gly Phe
 245 250 255
 Met Ser Gly Thr Leu Ala Ile Arg Lys Ala Asp Glu Gly Lys Trp Gln
 260 265 270
 Leu Val Gly Gly Asp Ile Gln Asn Ala Ile Val Gln Asn Ile Cys Met
 10 275 280 285
 Met Asp Asp Asn Lys Ile Ala Cys Glu Val Phe Gly Thr Pro Asn Gly
 290 295 300
 Val Asp Gly Arg Thr Arg Val Cys Val Ser Asp Ala Ser Val Phe Asp
 305 310 315 320
 15 Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly Gly Leu Ile Phe Asp Thr
 325 330 335
 Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu Tyr Ala Lys Phe Gly Gly
 340 345 350
 Ile Met Leu Arg Ser Lys Glu Ser Phe Ile Thr Ser Phe Ile Ser Pro
 20 355 360 365
 Thr Val Val Gln Gly Val Asp Val Tyr Thr Leu Ala Gly Lys Ile Arg
 370 375 380
 Ile Glu Ser Glu Thr Pro Val Ser Glu Val Leu Leu Phe Asp Leu Ala
 385 390 395 400
 25 Gly Arg Met Val Leu Arg Gln Thr Ile Asp Asn Lys Ile Tyr Ser Asp
 405 410 415
 Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly Ile Tyr Val Val Ser Val
 420 425 430
 Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val
 30 435 440 445

(2) INFORMATION FOR SEQ ID NO:113

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 308 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

15

Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly

1 5 10 15

Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys

20 25 30

20 Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu

35 40 45

Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe

50 55 60

Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp

25 65 70 75 80

Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn

85 90 95

Glu Glu Leu Asn Phe Ala Ala Glu Arg Arg Asp Phe Val Ser Pro Leu

100 105 110

30 Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp

115 120 125

Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu

130 135 140

Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe

35 145 150 155 160

Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln

251

165 170 175
Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp
180 185 190
Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln
5 195 200 205
Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser
210 215 220
Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser
225 230 235 240
10 Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro
245 250 255
Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val
260 265 270
Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile
15 275 280 285
Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr
290 295 300
Gly Asp Lys Lys
305

20

(2) INFORMATION FOR SEQ ID NO:114

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids
25 (B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

[illegible]

(2) INFORMATION FOR SEQ ID NO:115

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

15

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...540

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

```

Met Lys Thr Lys Val Leu Arg Lys Phe Val Val Ala Ala Phe Ala Val
1           5           10           15
Ala Thr Leu Cys Pro Leu Ala Gln Ala Gln Thr Met Gly Gly Asp Asp
25           20           25           30
Val Lys Val Val Gln Tyr Asn Gln Glu Lys Leu Val Gln Thr Arg Met
           35           40           45
Ser Val Ala Asp Asn Gly Trp Ile Tyr Val Met Thr His Ser Gly Tyr
           50           55           60
30 Asp Thr Gly Asn Ser Asn Val Lys Ile Phe Arg Ser Lys Asp Gln Gly
65           70           75           80
Ala Thr Tyr Gln Lys Leu Arg Asp Trp Asp Pro Ser Asp Asp Tyr Gln
           85           90           95
Phe Gln Asp Phe Asp Ile Val Val Thr Gly Lys Asn Glu Ser Asp Ile
35           100          105          110
Lys Ile Trp Ser Val Glu Leu Met Asn Lys Pro Gly Gly Tyr Lys Ser

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	115	120	125
	Arg Val Ala Val Phe Ser Arg Asp Ala Asn Ala Gln Asn Ala Lys Leu		
	130	135	140
	Val Tyr Lys Glu Asp Phe Ser Asn Val Gln Leu Tyr Asp Val Asp Ile		
5	145	150	155
	Ala Ser Asn Tyr Arg Ser Pro Ser Ser Leu Asn Asn Gly Gly Asn Pro		
	165	170	175
	Phe Ala Leu Ala Phe Ala Tyr Thr Gly Phe Asn Asn Thr His Lys Ile		
	180	185	190
10	Ser Phe Val Asp Tyr Val Phe Ser Leu Asn Gly Gly Gln Asn Phe Asn		
	195	200	205
	Lys Asn Leu Leu Phe Ser Gln Asp Gly Glu Lys Lys Ile Asp Lys Val		
	210	215	220
	Asp Leu Ser Leu Gly Ser Thr Ser Glu Ser Met Gly His Asn Ala Trp		
15	225	230	235
	Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Gln Gly Gly Lys Ser		
	245	250	255
	Asp Ile Gly Phe Leu Ser Asn Phe Val Asp Asn Asp Pro Glu Phe Gln		
	260	265	270
20	Trp Ser Gly Pro Ile Lys Val Ser Glu Ser Asp Met Ser Phe Ser Pro		
	275	280	285
	Lys Ile Gln Met Leu Leu Asp Glu Asp Asn Asn Thr Ile Asn Gly Glu		
	290	295	300
	Ser Cys His Asn Phe Met Ile Thr Tyr Ser Asp Tyr Asp Ser Glu Tyr		
25	305	310	315
	Ser Asp Trp Asp Ile Arg Tyr Val Tyr Pro Lys Lys Ser Phe Lys Tyr		
	325	330	335
	Glu Lys Gly Lys Thr Pro Thr Met Asp Asp Leu Val Glu Ala Phe Leu		
	340	345	350
30	Thr Ala Ser Tyr Gln Ser Glu Thr Asn Ser Gly Leu Gly Tyr Asp Lys		
	355	360	365
	Asn Ala Asn His Tyr Leu Ile Thr Tyr Ala Lys Lys Glu Glu Asn Gly		
	370	375	380
	Thr Asn Thr Leu Lys Tyr Arg Trp Ala Asn Tyr Asp Lys Ile His Asn		
35	385	390	395
	Lys Asp Leu Trp Ser Asp Thr Phe Thr Tyr Thr Ser Ser Ala Asn Ala		

255

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                                405                410                415
Leu Tyr Thr Pro Gln Val Asp Ile Asn Pro Thr Lys Gly Leu Val Cys
                                420                425                430
Trp Ser Trp Val Glu Tyr Leu Pro Gly Lys Arg Ile Val Trp Ser Asp
5      435                440                445
Thr Gln Trp Thr His Ala Asn Gly Val Glu Asp Ile Val Met Gln Glu
      450                455                460
Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala Gln Glu Tyr Ala Val Ile
465                470                475                480
10    Ser Leu Pro Thr Ala Ala Asn Cys Lys Ala Val Val Tyr Asp Met Gln
      485                490                495
Gly Arg Val Val Ala Glu Ala Ser Phe Ser Gly Asn Glu Tyr Arg Leu
      500                505                510
Asn Val Gln His Leu Ala Lys Gly Thr Tyr Ile Leu Lys Val Val Ser
15      515                520                525
Asp Thr Glu Arg Phe Val Glu Lys Leu Ile Val Glu
      530                535                540
```

(2) INFORMATION FOR SEQ ID NO:116

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

25

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

30

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...259

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

```

Met Lys Lys Thr Thr Leu Thr Gly Ser Ile Cys Ala Leu Leu Leu Phe
1           5           10           15
5  Leu Gly Leu Ser Ala Asn Ala Gln Ser Lys Leu Lys Ile Lys Ser Ile
    20           25           30
Glu Ala Ala Thr Thr Phe Ser Ser Ala Thr Ala Gly Asn Gly Phe Gly
    35           40           45
Gly Asn Ile Phe Gly Met Asp Met Ser Ile Arg Met Arg Val His His
10   50           55           60
Ser Ile Leu Pro Glu Gly Leu Asp Phe Ser Val Gly Ile His Glu Arg
65           70           75           80
Arg Ala His Trp Glu Glu Ala Gly Ser Pro Lys Leu Met Tyr Thr Asn
    85           90           95
15 Val Pro Ser Ile Ile Gly Ile Val Glu Lys Val Ile Val Phe Glu Asp
    100          105          110
Ala Glu Asp Phe Phe Asp Lys Lys Ala Leu Gly Arg Phe Leu Ile Ser
    115          120          125
Leu Gly Ile Ser Tyr Thr Lys His Leu Gly Ala Tyr Trp Gly Trp Thr
20   130          135          140
Asn Asp Ala His Ile Leu Phe Ser Pro Ile Pro Lys Ser Lys Val His
145          150          155          160
Tyr Asp Thr Tyr Thr Arg Ala Gly Ser Asp Leu Val Leu Gln Ser Glu
    165          170          175
25 Asp Val Ala Thr Val Ser Asn Gly Phe Ser Pro Gly Ile Gly Leu Lys
    180          185          190
Ser Ser Ile Trp Trp Lys Met Pro Ile Lys Ser Lys Tyr Asp Phe Arg
    195          200          205
Leu Gly Phe Ser Leu Gly Tyr Glu Tyr Leu Asn Leu Leu Tyr Pro Tyr
30   210          215          220
Arg Asn Phe Lys Leu Asp Gly Asn Lys Pro Leu Ser Ala Leu Ser Pro
225          230          235          240
Arg Met Asn His Ile Gly His Val Gly Phe Asn Phe Thr Val Gly Leu
    245          250          255
35 Trp Thr Asn

```


(2) INFORMATION FOR SEQ ID NO:117

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 271 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...271

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser
 1 5 10 15
 Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys
 25 20 25 30
 Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg
 35 40 45
 Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr
 50 55 60
 30 Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe
 65 70 75 80
 Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly
 85 90 95
 Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala
 35 100 105 110
 Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln

	115	120	125
	Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile		
	130	135	140
	Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg		
5	145	150	155
	Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp		
	165	170	175
	Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly		
	180	185	190
10	Gln Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala		
	195	200	205
	Ile Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met		
	210	215	220
	Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala		
15	225	230	235
	Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu		
	245	250	255
	Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro		
	260	265	270

20

(2) INFORMATION FOR SEQ ID NO:118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

30

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

35

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

```

5  Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
   1             5             10             15
   Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
      20             25             30
   Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
10      35             40             45
   Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
      50             55             60
   Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
   65             70             75             80
15  Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
      85             90             95
   Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
      100            105            110
   Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
20      115            120            125
   Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
      130            135            140
   Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
   145            150            155            160
25  Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
      165            170            175
   Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
      180            185            190
   Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
30      195            200            205
   Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
      210            215            220
   Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
   225            230            235            240
35  Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
      245            250            255

```

Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
 260 265 270

(2) INFORMATION FOR SEQ ID NO:119

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...400

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

Met Val Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val
 25 1 5 10 15
 Leu Leu Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu
 20 25 30
 Asp Asp Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val
 35 40 45
 30 Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr
 50 55 60
 Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly
 65 70 75 80
 Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser
 35 85 90 95
 Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe

	100	105	110
	Tyr Lys Pro Asn Thr Ile Val	Ile Ser Gly Ala Asp Asn Val Tyr Val	
	115	120	125
	Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp		
5	130	135	140
	Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe		
	145	150	155
	Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr		
	165	170	175
10	Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly		
	180	185	190
	Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe		
	195	200	205
	Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp		
15	210	215	220
	Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr		
	225	230	235
	His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala		
	245	250	255
20	Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly		
	260	265	270
	Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser		
	275	280	285
	Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu		
25	290	295	300
	Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn		
	305	310	315
	Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val		
	325	330	335
30	Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile		
	340	345	350
	Arg Ser Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro		
	355	360	365
	Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser		
35	370	375	380
	Ser Gly Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn		

385

390

395

400

(2) INFORMATION FOR SEQ ID NO:120

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

15

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...398

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu

1 5 10 15

25 Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp

20 25 30

Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp

35 40 45

Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val

30 50 55 60

Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser

65 70 75 80

Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg

85 90 95

35 Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys

100 105 110

Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp
 115 120 125
 Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser
 130 135 140
 5 Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr
 145 150 155 160
 Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn
 165 170 175
 Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr
 10 180 185 190
 Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn
 195 200 205
 Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser
 210 215 220
 15 Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His
 225 230 235 240
 Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr
 245 250 255
 Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys
 20 260 265 270
 Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys
 275 280 285
 Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn
 290 295 300
 25 Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu
 305 310 315 320
 Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln
 325 330 335
 Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser
 30 340 345 350
 Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg
 355 360 365
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly
 370 375 380
 35 Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 385 390 395

(2) INFORMATION FOR SEQ ID NO:121

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...207

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

Met Lys Arg Met Leu Leu Leu Leu Val Val Leu Leu Tyr Gly Ile Ala
 1 5 10 15
 Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp Ser Leu Gln Val
 25 20 25 30
 Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly Gly Phe Thr Tyr
 35 40 45
 Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu Glu Val Gly Leu
 50 55 60
 30 Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn Ala Asp Ser Phe
 65 70 75 80
 Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn Met Ser Ser Pro
 85 90 95
 Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala Asn Cys Tyr Met
 35 100 105 110
 Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp Gln Asn Ser Arg


```

115              120              125
His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser Asn Lys His Asn
130              135              140
Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val Ser Ile Tyr Thr
5  145              150              155              160
Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val Ala Tyr Glu Tyr
165              170              175
Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val Met Tyr Asp His
180              185              190
10 Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser Thr His Phe
195              200              205

```

(2) INFORMATION FOR SEQ ID NO:122

```

15      (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 771 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

20      (ii) MOLECULE TYPE: protein

      (iii) HYPOTHETICAL: YES

      (vi) ORIGINAL SOURCE:
25      (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...771

30      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

```

```

Met Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile
1              5              10              15
35 Ala Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu
20              25              30

```

	Thr	Glu	Tyr	Val	Asn	Pro	Phe	Ile	Gly	Thr	Ala	Asn	Tyr	Gly	Thr	Thr	
		35						40					45				
	Asn	Pro	Gly	Ala	Val	Leu	Pro	Asn	Gly	Leu	Met	Ser	Val	Thr	Pro	Phe	
		50					55					60					
5	Asn	Val	Ser	Gly	Ser	Thr	Glu	Asn	Arg	Phe	Asp	Lys	Asp	Ser	Arg	Trp	
	65					70				75					80		
	Trp	Ser	Ala	Pro	Tyr	Ser	Ala	Asp	Asn	Ser	Tyr	Cys	Ile	Gly	Phe	Ser	
					85					90					95		
	His	Val	Asn	Leu	Ser	Gly	Val	Gly	Cys	Pro	Glu	Leu	Ser	Gly	Ile	Leu	
10				100					105					110			
	Leu	Met	Ala	Thr	Ser	Gly	Thr	Phe	Asp	Pro	Asp	Tyr	Cys	Cys	Tyr	Gly	
		115						120					125				
	Ser	Ser	Leu	Ser	Arg	Glu	Tyr	Ala	Arg	Pro	Gly	Glu	Tyr	Lys	Ala	Val	
		130						135					140				
15	Leu	Asp	Lys	Tyr	Gly	Ile	Asp	Ala	Ala	Val	Thr	Val	Thr	Glu	Arg	Thr	
	145					150					155				160		
	Ala	Leu	Thr	Glu	Phe	Ala	Phe	Pro	Glu	Gly	Glu	Gly	His	Ile	Leu	Leu	
					165					170					175		
	Asn	Leu	Gly	Gln	Ala	Leu	Ser	Asn	Glu	Ser	Gly	Ala	Ser	Val	Arg	Phe	
20				180					185					190			
	Leu	Asn	Asp	Ser	Thr	Val	Val	Gly	Ser	Arg	Leu	Met	Gly	Thr	Phe	Cys	
		195						200					205				
	Tyr	Asn	Pro	Gln	Ala	Val	Phe	Arg	Gln	Tyr	Phe	Val	Leu	Gln	Val	Ser	
		210					215					220					
25	Arg	Arg	Pro	Ile	Ser	Ala	Gly	Tyr	Trp	Lys	Lys	Gln	Pro	Pro	Met	Thr	
	225					230					235				240		
	Val	Glu	Ala	Gln	Trp	Asp	Ser	Thr	Ala	Gly	Lys	Tyr	Lys	Gln	Tyr	Asp	
					245					250					255		
	Gly	Tyr	Lys	Arg	Glu	Met	Ser	Gly	Asp	Asp	Ile	Gly	Val	Arg	Phe	Ser	
30				260					265					270			
	Phe	Asn	Cys	Asp	Gln	Gly	Glu	Lys	Ile	Tyr	Val	Arg	Ser	Ala	Val	Ser	
		275						280					285				
	Phe	Val	Ser	Glu	Ala	Asn	Ala	Leu	Tyr	Asn	Leu	Glu	Ala	Glu	Gln	Glu	
		290					295					300					
35	Glu	Val	Phe	Lys	Ser	Val	Gly	Gly	Asn	Pro	Ala	Lys	Ala	Phe	Ser	Ala	
	305					310					315				320		

	Ile Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val	
	325	330 335
	Glu Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala	
	340	345 350
5	Leu Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly	
	355	360 365
	Glu Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp	
	370	375 380
	Arg Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro	
10	385	390 395 400
	Leu Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr	
	405	410 415
	Leu Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu	
	420	425 430
15	Tyr Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val	
	435	440 445
	Ile Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr	
	450	455 460
	Ala Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His	
20	465	470 475 480
	Pro Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro	
	485	490 495
	Leu Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr	
	500	505 510
25	Leu Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys	
	515	520 525
	Glu Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr	
	530	535 540
	Tyr Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser	
30	545	550 555 560
	Phe Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn	
	565	570 575
	Pro Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro	
	580	585 590
35	His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe	
	595	600 605

Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr
 610 615 620
 Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys
 625 630 635 640
 5 Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His
 645 650 655
 Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr
 660 665 670
 Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys
 10 675 680 685
 Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val
 690 695 700
 Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile
 705 710 715 720
 15 Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr
 725 730 735
 Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser
 740 745 750
 His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn
 20 755 760 765
 Arg Pro Arg
 770

(2) INFORMATION FOR SEQ ID NO:123

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 951 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...951

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

```

Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu Pro Val
1           5           10           15
10 Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu Arg Pro
           20           25           30
Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala Leu Ser
           35           40           45
Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile Pro Asp
15          50           55           60
Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser Met Arg
           65           70           75           80
Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile Val Glu
           85           90           95
20 Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg Ala Tyr
           100          105          110
Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu Glu Ala
           115          120          125
Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr Arg Tyr
25          130          135          140
Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe Lys Asp
           145          150          155          160
Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe Arg Thr
           165          170          175
30 Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu Gly Tyr
           180          185          190
Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met Phe Met
           195          200          205
Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro His Phe
35          210          215          220
Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp Ile Val

```

	225		230		235		240									
	Thr	Gly	Pro	Val	Asn	Leu	Val	Ile	Ala	Asp	Met	Pro	Leu	Pro	Ile	Gly
			245					250							255	
	Leu	Pro	Phe	Gly	Tyr	Phe	Pro	Phe	Ser	Asn	Lys	Tyr	Ser	Ser	Gly	Ile
5			260					265							270	
	Leu	Met	Pro	Thr	Tyr	Gly	Glu	Asp	Asn	Arg	Tyr	Gly	Phe	Tyr	Leu	Arg
			275					280						285		
	Asn	Gly	Gly	Tyr	Tyr	Phe	Ala	Phe	Ser	Asp	Tyr	Ile	Asp	Leu	Ala	Leu
			290					295						300		
10	Arg	Gly	Glu	Ile	Phe	Ser	Lys	Gly	Ser	Trp	Gly	Ile	Ser	Ala	Gln	Ser
	305						310				315				320	
	Lys	Tyr	Lys	Lys	Arg	Tyr	Lys	Tyr	Asn	Gly	Ser	Phe	Glu	Ala	Asn	Tyr
					325					330					335	
	Leu	Val	Ser	Lys	Ser	Gly	Asp	Lys	Tyr	Val	Pro	Gly	Asp	Tyr	Ser	Lys
15			340					345						350		
	Thr	Thr	Ser	Leu	Asn	Ile	Arg	Trp	Thr	His	Ser	Gln	Asp	Pro	Lys	Ala
			355					360						365		
	Asn	Pro	Leu	Gln	Thr	Leu	Ser	Ala	Asn	Val	Asn	Phe	Ala	Thr	Gly	Ser
			370					375						380		
20	Tyr	Phe	Gln	Asn	Ser	Leu	Asn	Thr	Thr	Tyr	Asp	Val	Asn	Ala	Arg	Thr
	385						390				395				400	
	Ala	Thr	Thr	Arg	Ser	Ser	Ala	Val	Ser	Tyr	Ser	Arg	Lys	Phe	Pro	Gly
					405					410					415	
	Thr	Pro	Phe	Ser	Ile	Thr	Gly	Ser	Met	Asp	Ile	Ser	Gln	Asn	Met	Arg
25			420					425						430		
	Asp	Thr	Thr	Val	Ser	Leu	Thr	Leu	Pro	Asn	Leu	Ser	Ile	Asn	Met	Ser
			435					440						445		
	Thr	Arg	Tyr	Pro	Phe	Lys	Arg	Lys	Thr	Arg	Val	Gly	Pro	Glu	Arg	Trp
			450					455						460		
30	Tyr	Glu	Lys	Leu	Ser	Val	Gly	Tyr	Ser	Gly	Gln	Leu	Arg	Asn	Ser	Ile
	465						470				475				480	
	Leu	Thr	Lys	Glu	Lys	Asp	Leu	Leu	Gln	Ser	Asn	Leu	Val	Arg	Asp	Trp
					485					490					495	
	Lys	Asn	Gly	Met	Arg	His	Ser	Val	Pro	Ile	Ser	Leu	Thr	Val	Pro	Leu
35			500					505						510		
	Leu	Asp	Tyr	Ile	Asn	Leu	Thr	Met	Gly	Val	Asn	Tyr	Asn	Glu	Trp	Trp

	515		520		525
	Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys Thr Phe				
	530		535		540
	Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp Tyr Ser				
5	545		550		555
	Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys Pro Trp				
		565		570	575
	Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His Arg Phe				
		580		585	590
10	Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys Arg Arg				
		595		600	605
	Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly Lys Leu				
		610		615	620
	His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly Ala Pro				
15	625		630		635
	Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn Asn Leu				
		645		650	655
	Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys Lys Ile				
		660		665	670
20	Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met Phe Ala				
		675		680	685
	Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu Arg Leu				
		690		695	700
	Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro Tyr Leu				
25	705		710		715
	Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr Lys Ser				
		725		730	735
	Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu Ile Ser				
		740		745	750
30	Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly				
		755		760	765
	Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys				
		770		775	780
	Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu				
35	785		790		795
	Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu Glu Arg				800

805 810 815
 Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser
 820 825 830
 Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala Thr Asp
 5 835 840 845
 Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg Val Thr
 850 855 860
 Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn Trp Ser
 865 870 875 880
 10 Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser
 885 890 895
 Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile Ser Ala
 900 905 910
 Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val Ile Ser
 15 915 920 925
 Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser Asn Arg
 930 935 940
 Pro Ile Thr Asn Thr Trp Tyr
 945 950

20

(2) INFORMATION FOR SEQ ID NO:124

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 581 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

```

5  Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser
   1             5             10             15
Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg
   20             25             30
Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro
10      35             40             45
Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met
   50             55             60
Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser
   65             70             75             80
15  Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg
   85             90             95
Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Unk
   100            105            110
Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu
20      115            120            125
Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe
   130            135            140
Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly
   145            150            155            160
25  Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile
   165            170            175
Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn
   180            185            190
Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu
30      195            200            205
Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly
   210            215            220
Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly
   225            230            235            240
35  Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile
   245            250            255

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Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala
 260 265 270
 Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile
 275 280 285
 5 Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys
 290 295 300
 Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe
 305 310 315 320
 Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met
 10 325 330 335
 Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro
 340 345 350
 Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg
 355 360 365
 15 Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly
 370 375 380
 Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu
 385 390 395 400
 Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser
 20 405 410 415
 Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile
 420 425 430
 Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn
 435 440 445
 25 Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro
 450 455 460
 Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu
 465 470 475 480
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys
 30 485 490 495
 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu
 500 505 510
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr
 515 520 525
 35 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His
 530 535 540

10 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 940 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

20 (A) ORGANISM: Porphyromonas gingivalis

(A) NAME/KEY: misc_feature
(B) LOCATION 1...940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

	Met	Asn	Lys	Phe	Tyr	Lys	Ser	Leu	Leu	Gln	Ser	Gly	Leu	Ala	Ala	Phe
	1				5					10					15	
30	Val	Ser	Met	Ala	Thr	Ala	Leu	Thr	Ala	Ser	Ala	Gln	Ile	Ser	Phe	Gly
				20					25					30		
	Gly	Glu	Pro	Leu	Ser	Phe	Ser	Ser	Arg	Ser	Ala	Gly	Thr	His	Ser	Phe
			35					40					45			
	Asp	Asp	Ala	Met	Thr	Ile	Arg	Leu	Thr	Pro	Asp	Phe	Asn	Pro	Glu	Asp
35		50					55					60				
	Leu	Ile	Ala	Gln	Ser	Arg	Trp	Gln	Ser	Gln	Arg	Asp	Gly	Arg	Pro	Val

	65		70		75		80									
	Arg	Ile	Gly	Gln	Val	Ile	Pro	Val	Asp	Val	Asp	Phe	Ala	Ser	Lys	Ala
			85						90						95	
	Ser	His	Ile	Ser	Ser	Ile	Gly	Asp	Val	Asp	Val	Tyr	Arg	Leu	Gln	Phe
5			100						105						110	
	Lys	Leu	Glu	Gly	Ala	Lys	Ala	Ile	Thr	Leu	Tyr	Tyr	Asp	Ala	Phe	Asn
			115						120					125		
	Ile	Pro	Glu	Gly	Gly	Arg	Leu	Tyr	Ile	Tyr	Thr	Pro	Asp	His	Glu	Ile
			130						135					140		
10	Val	Leu	Gly	Ala	Tyr	Thr	Asn	Ala	Thr	His	Arg	Arg	Asn	Gly	Ala	Phe
			145						150					155		160
	Ala	Thr	Glu	Pro	Val	Pro	Gly	Ser	Glu	Leu	Ile	Met	Asp	Tyr	Glu	Val
					165						170				175	
	Ser	Arg	Gly	Gly	Thr	Leu	Pro	Asp	Ile	Lys	Ile	Ser	Gly	Ala	Gly	Tyr
15			180						185					190		
	Ile	Phe	Asp	Lys	Val	Gly	Gly	Arg	Pro	Val	Thr	Asp	Asn	His	Tyr	Gly
			195						200					205		
	Ile	Gly	Glu	Asp	Asp	Ser	Asp	Ser	Asp	Cys	Glu	Ile	Asn	Ile	Asn	Cys
			210						215					220		
20	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys	Asn	Gly	Val	Val	Gln	Met
			225						230					235		240
	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met	Cys	Ser	Gly	Asn	Leu	Leu
					245						250				255	
	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu	Ile	Ile	Ser	Ala	Gly	His
25			260						265					270		
	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val	Thr	Gln	Ser	Glu	Leu	Asp
			275						280					285		
	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys	Arg	Gly	Cys	Ser	Asn	Gly
			290						295					300		
30	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile	Ile	Gly	Ala	Ser	Met	Lys
			305						310					315		320
	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp	Gly	Leu	Leu	Leu	Gln	Leu
					325						330				335	
	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val	Tyr	Tyr	Asn	Gly	Trp	Asp
35			340						345					350		
	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala	Gly	Ile	His	His	Pro	Ala

	355		360		365	
	Gly Asp Ala Met Lys Ile Ser Ile Leu Lys Lys Thr Pro Ala Leu Asn					
	370		375		380	
	Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly Thr Asp Asp His Phe Tyr					
5	385		390		395	400
	Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly Gly Ser Ser Gly Ser Ser					
		405		410		415
	Leu Phe Asn Gln Asn Lys His Val Val Gly Thr Leu Thr Gly Gly Ala					
		420		425		430
10	Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly Arg Leu Asn Ser His Trp					
		435		440		445
	Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser Arg Met Asp Ile Tyr Leu					
		450		455		460
	Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile Leu Asn Gly Thr Tyr Arg					
15	465		470		475	480
	Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro Arg Leu Leu Leu Gln Ser					
		485		490		495
	Thr Gly Asp Gln Val Glu Leu Asn Trp Thr Ala Val Pro Ala Asp Gln					
		500		505		510
20	Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His Ile Phe Arg Asn Gly Lys					
		515		520		525
	Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr Ser Asp Ala Ile Asp Glu					
		530		535		540
	Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr Glu Val Ser Ala Arg Phe					
25	545		550		555	560
	Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu Ser Tyr Lys Asp Thr Asp					
		565		570		575
	Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp Ile Gln Thr Lys Leu Lys					
		580		585		590
30	Pro Asp Val Thr Pro Leu Pro Gly Gly Gly Val Ser Leu Ser Trp Lys					
		595		600		605
	Val Pro Phe Leu Ser Gln Leu Val Ser Arg Phe Gly Glu Ser Pro Asn					
		610		615		620
	Pro Val Phe Lys Thr Phe Glu Val Pro Tyr Val Ser Ala Ala Ala Ala					
35	625		630		635	640
	Gln Thr Pro Asn Pro Pro Val Gly Val Val Ile Ala Asp Lys Phe Met					

					645					650					655	
	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile	Ala	Ala	Val	Tyr	Val	Met
					660					665					670	
	Pro	Ser	Ala	Pro	Asp	Ser	Thr	Phe	His	Leu	Phe	Leu	Lys	Ser	Asn	Thr
5					675					680					685	
	Asn	Arg	Arg	Leu	Gln	Lys	Val	Thr	Thr	Pro	Ser	Asp	Trp	Gln	Ala	Gly
					690					695					700	
	Thr	Trp	Leu	Arg	Ile	Asn	Leu	Asp	Lys	Pro	Phe	Pro	Val	Asn	Asn	Asp
	705					710					715				720	
10	His	Met	Leu	Phe	Ala	Gly	Ile	Arg	Met	Pro	Asn	Lys	Tyr	Lys	Leu	Asn
					725						730				735	
	Arg	Ala	Ile	Arg	Tyr	Val	Arg	Asn	Pro	Asp	Asn	Leu	Phe	Ser	Ile	Thr
					740					745				750		
	Gly	Lys	Lys	Ile	Ser	Tyr	Asn	Asn	Gly	Val	Ser	Phe	Glu	Gly	Tyr	Gly
15					755					760				765		
	Ile	Pro	Ser	Leu	Leu	Gly	Tyr	Met	Ala	Ile	Lys	Tyr	Leu	Val	Val	Asn
					770					775				780		
	Thr	Asp	Ala	Pro	Lys	Ile	Asp	Met	Ser	Leu	Val	Gln	Glu	Pro	Tyr	Ala
	785					790					795				800	
20	Lys	Gly	Thr	Asn	Val	Ala	Pro	Phe	Pro	Glu	Leu	Val	Gly	Ile	Tyr	Val
					805					810					815	
	Tyr	Lys	Asn	Gly	Thr	Phe	Ile	Gly	Thr	Gln	Asp	Pro	Ser	Val	Thr	Thr
					820					825				830		
	Tyr	Ser	Val	Ser	Asp	Gly	Thr	Glu	Ser	Asp	Glu	Tyr	Glu	Ile	Lys	Leu
25					835					840				845		
	Val	Tyr	Lys	Gly	Ser	Gly	Ile	Ser	Asn	Gly	Val	Ala	Gln	Ile	Glu	Asn
					850					855				860		
	Asn	Asn	Ala	Val	Val	Ala	Tyr	Pro	Ser	Val	Val	Thr	Asp	Arg	Phe	Ser
	865					870					875				880	
30	Ile	Lys	Asn	Ala	His	Met	Val	His	Ala	Ala	Ala	Leu	Tyr	Ser	Leu	Asp
					885					890					895	
	Gly	Lys	Gln	Val	Arg	Ser	Trp	Asn	Asn	Leu	Arg	Asn	Gly	Val	Thr	Phe
					900					905				910		
	Ser	Val	Gln	Gly	Leu	Thr	Ala	Gly	Thr	Tyr	Met	Leu	Val	Met	Gln	Thr
35					915					920				925		
	Ala	Asn	Gly	Pro	Val	Ser	Gln	Lys	Ile	Val	Lys	Gln				

930

935

940

(2) INFORMATION FOR SEQ ID NO:126

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1282 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1282

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

```

Met Arg Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly
1           5           10           .   15
25 Leu Gln Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu
           20           25           30
Pro Ser Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu
           35           40           45
Val Val Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln
30           50           55           60
Val Phe Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu
65           70           75           80
Gly Glu Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu
           85           90           95
35 Phe Ser Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe
           100          105          110

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Asp Asn Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu
 115 120 125
 Pro Glu Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp
 130 135 140
 5 Tyr Tyr Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser
 145 150 155 160
 Gln Asp Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr
 165 170 175
 Pro Phe Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys
 10 180 185 190
 Ile Glu Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys
 195 200 205
 Asn Thr Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr
 210 215 220
 15 Glu Ala Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg
 225 230 235 240
 Gly Thr Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln
 245 250 255
 Asn Cys Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln
 20 260 265 270
 Gln Pro His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr
 275 280 285
 Asn Gly Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser
 290 295 300
 25 Phe Pro Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn
 305 310 315 320
 Phe Ile Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp
 325 330 335
 Gly Lys Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr
 30 340 345 350
 Leu Ala Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn
 355 360 365
 Val Ser Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser
 370 375 380
 35 Asp Tyr Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu
 385 390 395 400

Phe Ile Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu
 405 410 415
 Ile Glu Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His
 420 425 430
 5 Lys Asn Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu
 435 440 445
 Arg Leu Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile
 450 455 460
 Leu Lys Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu
 10 465 470 475 480
 Asn Asn Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr
 485 490 495
 Val Trp Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg
 500 505 510
 15 Leu Asn Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser
 515 520 525
 Ser Ala Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr
 530 535 540
 Thr Tyr Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg
 20 545 550 555 560
 Ala Thr Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu
 565 570 575
 Phe Tyr Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val
 580 585 590
 25 Val Gly Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp
 595 600 605
 Thr Tyr Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn
 610 615 620
 Ile Met Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn
 30 625 630 635 640
 Asn Thr Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu
 645 650 655
 Lys Ile Pro Glu Lys Gly Val Leu His Phe Thr Asn Asn Gly Ser Ile
 660 665 670
 35 Gln Val Met Ser Gly Gly Thr Leu Glu Ile Gly Asn Gln Ala Lys Ile
 675 680 685

Ser Gly Glu Thr Gly Ala Asn Pro Thr Phe Ile Thr Val Tyr Gly Asp
 690 695 700
 Gly Leu Ala Ile Asn Lys Gln Val Glu Ile Asp Asn Ile Asp Arg Leu
 705 710 715 720
 5 Asn Leu Phe Ser Thr His Ser Val Met Pro Lys Phe His Phe Asp Ser
 725 730 735
 Val Lys Phe Asn Ser Ala Pro Leu Tyr Thr Thr Asn Cys Ile Val Glu
 740 745 750
 Ile Ser Asn Cys Glu Phe Thr Asn Arg Ser Asp Ile Ile Ser Lys Asn
 10 755 760 765
 Cys Asp Leu Ser Val Glu Asn Ser Met Phe Ser Ser Ser Gly Ile Thr
 770 775 780
 Val Phe Lys Pro Met Ala Thr Ser Ser Ile Thr Gly Leu Ser Thr Lys
 785 790 795 800
 15 Ala Lys Ile Thr Asp Asn Thr Phe Phe Ala Thr Gly Asn Phe Ala Tyr
 805 810 815
 His Ile Thr Asn Thr Pro Gly Leu Thr Ala Thr Ser Asn Ala Ala Ile
 820 825 830
 Lys Leu Asp Asn Ile Pro Glu Tyr Tyr Ile Ser Gly Asn Lys Ile Val
 20 835 840 845
 Asn Cys Asp Glu Ala Leu Val Leu Asn Asn Ser Gly Asn Arg Thr Asn
 850 855 860
 Arg Leu His Asn Ile Thr Arg Asn Val Ile Lys Asn Cys Arg Ile Gly
 865 870 875 880
 25 Ser Thr Leu Tyr Asn Ser Tyr Gly Ile Tyr Asn Arg Asn Lys Ile Ser
 885 890 895
 Asn Asn His Ile Gly Val Arg Leu Leu Asn Asn Ser Cys Phe Tyr Phe
 900 905 910
 Asp Asn Ala Pro Val Ile Asn Glu Glu Asp Lys Gln Thr Phe Ile Ser
 30 915 920 925
 Asn Arg Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn
 930 935 940
 Phe His Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr
 945 950 955 960
 35 Asn Asp Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp
 965 970 975

Gly Asn Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp
 980 985 990
 Leu Phe Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser
 995 1000 1005
 5 Gly Asn Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys
 1010 1015 1020
 Ile Gly Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met
 1025 1030 1035 1040
 Val Glu Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu
 10 1045 1050 1055
 Leu Phe Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys
 1060 1065 1070
 Asp Tyr Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe
 1075 1080 1085
 15 Pro Thr Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn
 1090 1095 1100
 Tyr Gln Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile
 1105 1110 1115 1120
 Ser Tyr Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr
 20 1125 1130 1135
 Trp Asn Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn
 1140 1145 1150
 Ile Leu Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val
 1155 1160 1165
 25 Lys Asn Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu
 1170 1175 1180
 Pro Pro Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile
 1185 1190 1195 1200
 Ser Ile Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr
 30 1205 1210 1215
 Thr Asp Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly
 1220 1225 1230
 Ala Ser Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr
 1235 1240 1245
 35 Tyr Ser Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu
 1250 1255 1260

Val Thr Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg
 1265 1270 1275 1280
 Ile Lys

5

(2) INFORMATION FOR SEQ ID NO:127

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 925 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

25

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile

1 5 10 15

Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser

20 25 30

30 Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile

35 40 45

Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu

50 55 60

Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser

35 65 70 75 80

Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile

	85	90	95
	Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile		
	100	105	110
	Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr		
5	115	120	125
	Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile		
	130	135	140
	Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr		
	145	150	155
10	Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys		
	165	170	175
	Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe		
	180	185	190
	Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu		
15	195	200	205
	Pro Ala Thr Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg		
	210	215	220
	Leu Thr Trp Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn		
	225	230	235
20	Glu Glu Leu Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu		
	245	250	255
	Leu Ala Gln Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr		
	260	265	270
	Tyr Ser Leu Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala		
25	275	280	285
	Val Tyr Asp Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His		
	290	295	300
	Tyr Ala Thr Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val		
	305	310	315
30	Pro Asn Gly Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp		
	325	330	335
	Gly His Tyr Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly		
	340	345	350
	His Cys Ser Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr		
35	355	360	365
	Pro Asp Asn Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val		

	370		375		380	
	Lys Tyr Trp Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr					
	385		390		395	400
	Ala Val Met Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile					
5		405		410		415
	Leu Phe Glu Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu					
		420		425		430
	Arg Thr Ile Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His					
		435		440		445
10	Tyr Asn Cys Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val					
		450		455		460
	Phe Gly Thr Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val					
		465		470		475
	Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn					
15		485		490		495
	Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala					
		500		505		510
	Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp					
		515		520		525
20	Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp					
		530		535		540
	Gln Val Glu Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile					
		545		550		555
	Glu Ser Gln Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp					
25		565		570		575
	Ile Ile Leu Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp					
		580		585		590
	Leu Leu Ile Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro					
		595		600		605
30	Trp Thr Met Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser					
		610		615		620
	Tyr Leu Pro Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr					
		625		630		635
	Pro Arg Leu Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln					
35		645		650		655
	Asp Ala Val Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr					

	660	665	670
	Gly Thr Ala Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr		
	675	680	685
	Ala Lys Ala Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala		
5	690	695	700
	Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe		
	705	710	715
	Phe Leu Leu Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val		
	725	730	735
10	Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys		
	740	745	750
	Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr		
	755	760	765
	Asp Asp Lys Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn		
15	770	775	780
	Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile		
	785	790	795
	Asp Glu Thr Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys		
	805	810	815
20	Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp		
	820	825	830
	Lys Leu Asn Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr		
	835	840	845
	Ser Leu Lys Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu		
25	850	855	860
	Gly Leu Ser Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly		
	865	870	875
	Ile Cys Ile Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp		
	885	890	895
30	Val Ser Arg Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly		
	900	905	910
	Asn Lys Thr Thr Thr Glu Lys Val Glu Ile Lys Arg Pro		
	915	920	925

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 922 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15

(B) LOCATION 1...922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

```

Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
20 1          5          10          15
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
          20          25          30
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
          35          40          45 . .
25 Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
          50          55          60
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
65          70          75          80
Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
30          85          90          95
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
          100          105          110
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
          115          120          125
35 His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
          130          135          140

```


	Val	Leu	Leu	Phe	Asp	Asp	Ser	Ile	Thr	Gly	Lys	Pro	Thr	Pro	Leu	Val	
	145					150					155					160	
	Trp	Arg	Arg	Arg	Ile	Val	Asp	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	
					165					170						175	
5	Trp	Arg	His	Tyr	Lys	Val	Thr	Asp	Ser	His	Thr	Glu	Phe	Leu	Lys	Leu	
					180				185						190		
	Asp	Asp	Val	Thr	Val	Tyr	Arg	Ser	Ile	Glu	Gly	Pro	Glu	Pro	Ala	Thr	
					195				200				205				
	Asp	Phe	Thr	Val	Ile	Asn	Ile	Gly	Gln	Asn	Val	Gly	Arg	Leu	Thr	Trp	
10		210						215					220				
	Asn	Tyr	Pro	Glu	Asp	Tyr	Gln	Pro	Glu	Gly	Lys	Gly	Asn	Glu	Glu	Leu	
	225					230					235					240	
	Gln	Leu	Ser	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Thr	Leu	Leu	Ala	Gln	
					245					250						255	
15	Ile	Lys	Asp	Val	Ser	Ile	Leu	Glu	Tyr	Val	Asp	Ser	Thr	Tyr	Ser	Leu	
					260					265					270		
	Arg	Asp	Asn	Pro	Leu	Gln	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asp	
					275					280					285		
	Glu	Ser	Ile	Glu	Ser	Ser	Thr	Val	Cys	Gly	Thr	Leu	His	Tyr	Ala	Thr	
20		290						295					300				
	Asp	Ala	Ile	Leu	Tyr	Glu	Asn	Phe	Glu	Asn	Gly	Pro	Val	Pro	Asn	Gly	
	305					310					315					320	
	Trp	Leu	Val	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Phe	Ser	Trp	Gly	His	Tyr	
					325					330						335	
25	Leu	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly	His	Cys	Ser	
					340					345					350		
	Leu	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr	Pro	Asp	Asn	
					355					360					365		
	Tyr	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val	Lys	Tyr	Trp	
30		370						375					380				
	Val	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr	Ala	Val	Met	
	385					390					395					400	
	Ala	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile	Leu	Phe	Glu	
					405					410						415	
35	Glu	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	
					420					425						430	

	Asn	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asn	Cys	
				435					440					445			
	Thr	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val	Phe	Gly	Thr	
			450				455					460					
5	Pro	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	
	465					470				475					480		
	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	
					485					490					495		
	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	Gly	Tyr	Asn	
10				500					505					510			
	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	
			515				520					525					
	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu	
			530				535				540						
15	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	
	545					550				555					560		
	Ser	Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu	
				565					570					575			
	Tyr	Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile	
20				580					585					590			
	Asp	Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met	
			595				600						605				
	Tyr	Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro	
		610					615				620						
25	Met	Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu	
	625					630				635					640		
	Glu	Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val	
				645						650				655			
	Tyr	Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	
30				660					665					670			
	Val	Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala	
			675					680					685				
	Asn	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys	
		690					695				700						
35	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu	
	705					710					715				720		

Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro
 725 730 735
 Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu
 740 745 750
 5 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys
 755 760 765
 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
 770 775 780
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
 10 785 790 795 800
 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
 805 810 815
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
 820 825 830
 15 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
 835 840 845
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
 850 855 860
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
 20 865 870 875 880
 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
 885 890 895
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
 900 905 910
 25 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
 915 920

(2) INFORMATION FOR SEQ ID NO:129

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 921 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyrromonas gingivalis*

5

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...921

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

```

Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp
1           5           10           15
Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala
15           20           25           30
Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser
           35           40           45
Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp
           50           55           60
20 Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro
           65           70           75           80
Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile
           85           90           95
Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys
25           100          105          110
Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His
           115          120          125
Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val
           130          135          140
30 Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp
           145          150          155          160
Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp
           165          170          175
Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp
35           180          185          190
Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp

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	195	200	205
	Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn		
	210	215	220
	Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln		
5	225	230	235 240
	Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln Ile		
	245	250	255
	Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu Arg		
	260	265	270
10	Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp Glu		
	275	280	285
	Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr Asp		
	290	295	300
	Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly Trp		
15	305	310	315 320
	Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr Leu		
	325	330	335
	Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser Leu		
	340	345	350
20	Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn Tyr		
	355	360	365
	Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp Val		
	370	375	380
	Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met Ala		
25	385	390	395 400
	Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu Glu		
	405	410	415
	Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile Asn		
	420	425	430
30	Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys Thr		
	435	440	445
	Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr Pro		
	450	455	460
	Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu		
35	465	470	475 480
	Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro		

	485	490	495
	Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn Ile		
	500	505	510
	Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu		
5	515	520	525
	Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu Val		
	530	535	540
	Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser		
	545	550	555
10	Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu Tyr		
	565	570	575
	Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile Asp		
	580	585	590
	Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met Tyr		
15	595	600	605
	Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro Met		
	610	615	620
	Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu Glu		
	625	630	635
20	Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val Tyr		
	645	650	655
	Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Val		
	660	665	670
	Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala Asn		
25	675	680	685
	Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys Tyr		
	690	695	700
	Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu Leu		
	705	710	715
30	Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro Val		
	725	730	735
	Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys		
	740	745	750
	Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Lys		
35	755	760	765
	Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu		

```

              770              775              780
Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr
785              790              795              800
Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala Val
5              805              810              815
Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn Tyr
              820              825              830
Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys Ile
              835              840              845
10 Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser Arg
              850              855              860
Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile Leu
865              870              875              880
Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg Leu
15              885              890              895
Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr Thr
              900              905              910
Thr Glu Lys Val Glu Ile Lys Arg Pro
              915              920

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20

(2) INFORMATION FOR SEQ ID NO:130

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1226 amino acids

25

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

35

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

5	Met	Met	Lys	Arg	Tyr	Thr	Ile	Ile	Leu	Ala	Val	Phe	Leu	Leu	Phe	Cys
	1				5					10					15	
	Thr	Val	Phe	Thr	Phe	Gln	Ile	Lys	Ala	Arg	Pro	Tyr	Glu	Arg	Phe	Ala
				20					25					30		
	Asp	Val	Glu	Lys	Pro	Trp	Ile	Gln	Lys	His	Ser	Met	Asp	Ser	Lys	Leu
10			35					40					45			
	Val	Pro	Ala	Asn	Lys	Gly	Asn	Leu	Ile	Gln	Ala	Glu	Ile	Val	Tyr	Gln
			50				55					60				
	Ser	Val	Ser	Glu	His	Ser	Asp	Leu	Val	Ile	Ser	Pro	Val	Asn	Glu	Ile
	65					70				75					80	
15	Arg	Pro	Ala	Asn	Arg	Phe	Pro	Ser	His	Arg	Lys	Ser	Phe	Phe	Ala	Glu
					85					90					95	
	Asn	Leu	Arg	Ala	Ser	Pro	Pro	Val	Val	Pro	Val	Ala	Val	Asp	Lys	Tyr
				100					105					110		
	Ala	Val	Pro	Val	Ala	Asn	Pro	Met	Asp	Pro	Glu	Asn	Pro	Asn	Ala	Trp
20			115					120					125			
	Asp	Val	Thr	Leu	Lys	Ile	Thr	Thr	Lys	Ala	Val	Thr	Val	Pro	Val	Asp
			130				135					140				
	Val	Val	Met	Val	Ile	Asp	Gln	Ser	Ser	Ser	Met	Gly	Gly	Gln	Asn	Ile
	145				150					155					160	
25	Ala	Arg	Leu	Lys	Ser	Ala	Ile	Ala	Ser	Gly	Gln	Arg	Phe	Val	Lys	Lys
					165				170						175	
	Met	Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val
				180					185				190			
	Ser	Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr
30			195					200					205			
	Ala	Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr
			210				215					220				
	His	Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser
	225				230					235					240	
35	Thr	Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr
					245				250						255	

2

Leu Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp
 545 550 555 560
 Gly Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu
 565 570 575
 5 Ala His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly
 580 585 590
 His Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu
 595 600 605
 Gln Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp
 10 610 615 620
 Gly Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro
 625 630 635 640
 Gly Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe
 645 650 655
 15 Ala Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln
 660 665 670
 Ser Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu
 675 680 685
 Thr Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro
 20 690 695 700
 Ala Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly
 705 710 715 720
 Asn Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser
 725 730 735
 25 Gln Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly
 740 745 750
 Thr Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu
 755 760 765
 Phe Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe
 30 770 775 780
 Tyr Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser
 785 790 795 800
 Trp Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn
 805 810 815
 35 Asp Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn
 820 825 830

	Gly	Asp	Lys	Trp	Arg	Pro	Ala	Pro	Tyr	Ala	Pro	Asp	Thr	Glu	Leu	Gln	
			835					840						845			
	Lys	Phe	Lys	Gly	Tyr	Gln	Ile	Thr	Asn	Asp	Val	Gln	Ala	Gln	Pro	Thr	
			850				855					860					
5	Gly	Val	Tyr	Ser	Phe	Lys	Gly	Met	Ile	Cys	Val	Cys	Asp	Ala	Phe	Leu	
							870					875				880	
	Asn	Leu	Thr	Arg	Thr	Ser	Gly	Val	Asn	Tyr	Ser	Gly	Ala	Asn	Leu	Ile	
							885				890				895		
	Gly	Asn	Ser	Tyr	Thr	Gly	Ala	Ile	Asp	Ile	Lys	Gln	Gly	Ile	Val	Phe	
10				900					905						910		
	Pro	Pro	Glu	Val	Glu	Gln	Thr	Val	Tyr	Leu	Phe	Asn	Thr	Gly	Thr	Arg	
				915					920						925		
	Asp	Gln	Trp	Arg	Lys	Leu	Asn	Gly	Ser	Thr	Val	Ser	Gly	Tyr	Arg	Ala	
							930						940				
15	Gly	Gln	Tyr	Leu	Ser	Val	Pro	Lys	Asn	Thr	Ala	Gly	Gln	Asp	Asn	Leu	
							945					955				960	
	Pro	Asp	Arg	Ile	Pro	Ser	Met	His	Ser	Phe	Leu	Val	Lys	Met	Gln	Asn	
							965				970				975		
	Gly	Ala	Ser	Cys	Thr	Leu	Unk	Ile	Leu	Tyr	Asp	Lys	Leu	Leu	Lys	Asn	
20				980					985						990		
	Thr	Thr	Val	Asn	Asn	Gly	Asn	Gly	Thr	Gln	Ile	Thr	Trp	Arg	Ser	Gly	
				995					1000						1005		
	Asn	Ser	Gly	Ser	Ala	Asn	Met	Pro	Ser	Leu	Val	Met	Asp	Val	Leu	Gly	
			1010					1015					1020				
25	Asn	Glu	Ser	Ala	Asp	Arg	Leu	Trp	Ile	Phe	Thr	Asp	Gly	Gly	Leu	Ser	
							1025					1035				1040	
	Phe	Gly	Phe	Asp	Asn	Gly	Trp	Asp	Gly	Arg	Lys	Leu	Thr	Glu	Lys	Gly	
							1045				1050				1055		
	Leu	Ser	Gln	Leu	Tyr	Ala	Met	Ser	Asp	Ile	Gly	Asn	Asp	Lys	Phe	Gln	
30				1060					1065						1070		
	Val	Ala	Gly	Val	Pro	Glu	Leu	Asn	Asn	Leu	Leu	Ile	Gly	Phe	Asp	Ala	
				1075					1080						1085		
	Asp	Lys	Asp	Gly	Gln	Tyr	Thr	Leu	Glu	Phe	Ala	Leu	Ser	Asp	His	Phe	
				1090					1095					1100			
35	Ala	Lys	Gly	Ala	Val	Tyr	Leu	His	Asp	Leu	Gln	Ser	Gly	Ala	Lys	His	
				1105				1110					1115			1120	

Arg Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp
 1125 1130 1135
 Ser Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp
 1140 1145 1150
 5 Asp Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn
 1155 1160 1165
 Gln Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys
 1170 1175 1180
 Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys
 10 1185 1190 1195 1200
 Val Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr
 1205 1210 1215
 Asn Asp Val His Lys Val Leu Val Glu Tyr
 1220 1225

15

(2) INFORMATION FOR SEQ ID NO:131

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1225 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

30 (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

35

Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys Thr

	1		5		10		15									
	Val	Phe	Thr	Phe	Gln	Ile	Lys	Ala	Arg	Pro	Tyr	Glu	Arg	Phe	Ala	Asp
				20				25						30		
	Val	Glu	Lys	Pro	Trp	Ile	Gln	Lys	His	Ser	Met	Asp	Ser	Lys	Leu	Val
5			35					40						45		
	Pro	Ala	Asn	Lys	Gly	Asn	Leu	Ile	Gln	Ala	Glu	Ile	Val	Tyr	Gln	Ser
			50					55					60			
	Val	Ser	Glu	His	Ser	Asp	Leu	Val	Ile	Ser	Pro	Val	Asn	Glu	Ile	Arg
	65					70					75				80	
10	Pro	Ala	Asn	Arg	Phe	Pro	Ser	His	Arg	Lys	Ser	Phe	Phe	Ala	Glu	Asn
					85					90					95	
	Leu	Arg	Ala	Ser	Pro	Pro	Val	Val	Pro	Val	Ala	Val	Asp	Lys	Tyr	Ala
			100						105					110		
	Val	Pro	Val	Ala	Asn	Pro	Met	Asp	Pro	Glu	Asn	Pro	Asn	Ala	Trp	Asp
15			115						120					125		
	Val	Thr	Leu	Lys	Ile	Thr	Thr	Lys	Ala	Val	Thr	Val	Pro	Val	Asp	Val
		130						135					140			
	Val	Met	Val	Ile	Asp	Gln	Ser	Ser	Ser	Met	Gly	Gly	Gln	Asn	Ile	Ala
	145					150					155				160	
20	Arg	Leu	Lys	Ser	Ala	Ile	Ala	Ser	Gly	Gln	Arg	Phe	Val	Lys	Lys	Met
					165					170				175		
	Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val	Ser
			180						185					190		
	Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr	Ala
25			195						200					205		
	Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr	His
		210						215					220			
	Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser	Thr
	225					230					235				240	
30	Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr	Glu
					245					250				255		
	Gln	Tyr	Pro	Val	Lys	Asn	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys	Thr
			260						265					270		
	Gly	Asn	Ala	Asn	Asp	Pro	Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile	Asn
35			275						280					285		
	Phe	Pro	Thr	Asn	Tyr	Val	Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr	Pro

	290		295		300
	Asn Tyr Pro Thr His Ser Ser Lys Val Gly Arg Arg Asn Leu Pro Glu				
	305		310		315 320
	Ser Lys Phe Asp Tyr Ser Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly				
5		325		330	335
	Val Ala Gly Ala Leu Val Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr				
		340		345	350
	Tyr Tyr Phe Pro Cys Asn Ala Ala Ile Asn Glu Ala Gln Phe Ala Lys				
		355		360	365
10	Asn Ser Gly Tyr Thr Ile His Thr Ile Gly Tyr Asp Leu Gly Asp Phe				
		370		375	380
	Ala Leu Ala Asn Asn Ser Leu Lys Leu Thr Ala Thr Asp Glu Asn His				
		385		390	395 400
	Phe Phe Thr Ala Thr Pro Ala Asn Leu Ala Ala Ala Phe Asp Asn Ile				
15		405		410	415
	Ala Gln Thr Ile Asn Ile Gly Ile Gln Arg Gly Glu Val Thr Asp Phe				
		420		425	430
	Val Ala Pro Gly Phe Ile Val Lys Asn Leu Thr Gln Ser Gly Asp Val				
		435		440	445
20	Thr His Leu Leu Asn Val Ser Asn Gly Thr Val His Tyr Asp Val Ser				
		450		455	460
	Thr Lys Lys Leu Thr Trp Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu				
		465		470	475 480
	Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn				
25		485		490	495
	Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly				
		500		505	510
	Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn				
		515		520	525
30	Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys Leu				
		530		535	540
	Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp Gly				
		545		550	555 560
	Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu Ala				
35		565		570	575
	His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly His				

		580				585				590						
	Ile	Val	Pro	Lys	Trp	Ile	Lys	Leu	Asp	Lys	Thr	Thr	Glu	Ala	Leu	Gln
				595				600					605			
	Tyr	Tyr	Ser	Val	Pro	Pro	Thr	Asn	Thr	Val	Ile	Thr	Thr	Ala	Asp	Gly
5		610					615					620				
	Lys	Arg	Tyr	Arg	Phe	Val	Glu	Val	Pro	Gly	Ser	Thr	Pro	Asn	Pro	Gly
	625					630					635				640	
	Gln	Ile	Gly	Ile	Ser	Trp	Lys	Lys	Pro	Ala	Gly	Asn	Ala	Tyr	Phe	Ala
				645						650				655		
10	Tyr	Lys	Leu	Leu	Asn	Tyr	Trp	Met	Gly	Gly	Thr	Thr	Asp	Gln	Gln	Ser
				660					665					670		
	Glu	Trp	Asp	Val	Thr	Ser	Asn	Trp	Thr	Gly	Ala	Gln	Val	Pro	Leu	Thr
				675					680					685		
	Gly	Glu	Asp	Val	Glu	Phe	Ala	Thr	Thr	Glu	Asn	Phe	Gly	Ser	Pro	Ala
15		690					695					700				
	Val	Ala	Asp	Leu	His	Val	Pro	Thr	Thr	Asn	Pro	Lys	Ile	Ile	Gly	Asn
	705					710					715				720	
	Leu	Ile	Asn	Asn	Ser	Asp	Lys	Asp	Leu	Val	Val	Thr	Thr	Ser	Ser	Gln
				725						730					735	
20	Leu	Thr	Ile	Asn	Gly	Val	Val	Glu	Asp	Asn	Asn	Pro	Asn	Val	Gly	Thr
				740					745					750		
	Ile	Val	Val	Lys	Ser	Ser	Lys	Asp	Asn	Pro	Thr	Gly	Thr	Leu	Leu	Phe
				755					760					765		
	Ala	Asn	Pro	Gly	Tyr	Asn	Gln	Asn	Val	Gly	Gly	Thr	Val	Glu	Phe	Tyr
25		770					775					780				
	Asn	Gln	Gly	Tyr	Asp	Cys	Ala	Asp	Cys	Gly	Met	Tyr	Arg	Arg	Ser	Trp
	785					790					795				800	
	Gln	Tyr	Phe	Gly	Ile	Pro	Val	Asn	Glu	Ser	Gly	Phe	Pro	Ile	Asn	Asp
				805						810					815	
30	Val	Gly	Gly	Asn	Glu	Thr	Val	Asn	Gln	Trp	Val	Glu	Pro	Phe	Asn	Gly
				820					825					830		
	Asp	Lys	Trp	Arg	Pro	Ala	Pro	Tyr	Ala	Pro	Asp	Thr	Glu	Leu	Gln	Lys
				835					840					845		
	Phe	Lys	Gly	Tyr	Gln	Ile	Thr	Asn	Asp	Val	Gln	Ala	Gln	Pro	Thr	Gly
35		850						855						860		
	Val	Tyr	Ser	Phe	Lys	Gly	Met	Ile	Cys	Val	Cys	Asp	Ala	Phe	Leu	Asn

	865		870		875		880
	Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly						
		885		890		895	
	Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe Pro						
5		900		905		910	
	Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp						
		915		920		925	
	Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly						
		930		935		940	
10	Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro						
	945		950		955		960
	Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly						
		965		970		975	
	Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr						
15		980		985		990	
	Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn						
		995		1000		1005	
	Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly Asn						
		1010		1015		1020	
20	Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe						
	1025		1030		1035		1040
	Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu						
		1045		1050		1055	
	Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln Val						
25		1060		1065		1070	
	Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp						
		1075		1080		1085	
	Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala						
		1090		1095		1100	
30	Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg						
	1105		1110		1115		1120
	Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser						
		1125		1130		1135	
	Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp						
35		1140		1145		1150	
	Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln						

1155 1160 1165
 Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu
 1170 1175 1180
 Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val
 5 1185 1190 1195 1200
 Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn
 1205 1210 1215
 Asp Val His Lys Val Leu Val Glu Tyr
 1220 1225

10

(2) INFORMATION FOR SEQ ID NO:132

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 425 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

30

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe
 1 5 10 15
 Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly
 20 25 30
 35 Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His
 35 40 45

	Ala	Val	Arg	Ser	Ser	Ser	Pro	Phe	Asp	Phe	Met	Ser	Ser	Arg	Thr	Arg
	50						55					60				
	Val	Arg	Gly	Glu	Leu	Glu	Arg	Ser	Phe	Gly	Asn	Ser	Lys	Val	Ala	Val
	65				70					75				80		
5	Ser	Val	Asn	Ala	Thr	Tyr	Asn	Ala	Leu	Leu	Lys	Asp	Glu	Thr	Gly	Leu
					85					90				95		
	Arg	Leu	Arg	Glu	Ala	Phe	Phe	Glu	His	Gln	Glu	Glu	His	Trp	Gly	Leu
					100					105				110		
	Arg	Leu	Gly	Arg	Gln	Ile	Val	Ile	Trp	Gly	Ala	Ala	Asp	Gly	Val	Arg
10			115						120					125		
	Ile	Thr	Asp	Leu	Ile	Ser	Pro	Met	Asp	Met	Thr	Glu	Phe	Leu	Ala	Gln
			130						135					140		
	Asp	Tyr	Asp	Asp	Ile	Arg	Met	Pro	Val	Asn	Ala	Leu	Arg	Phe	Ser	Val
	145				150					155					160	
15	Phe	Asn	Glu	Ser	Met	Lys	Val	Glu	Val	Val	Val	Leu	Pro	Val	Phe	Glu
					165					170					175	
	Gly	Tyr	Arg	Leu	Pro	Val	Asp	Pro	Arg	Asn	Pro	Trp	Asn	Ile	Phe	Ser
					180					185				190		
	Leu	Ser	Pro	Ile	Ala	Gln	Gly	Met	Asn	Ile	Val	Trp	Lys	Glu	Glu	Ala
20			195						200					205		
	Gly	Lys	Pro	Ala	Phe	Lys	Val	Ala	Asn	Ile	Glu	Tyr	Gly	Ala	Arg	Trp
			210						215					220		
	Ser	Thr	Thr	Leu	Ser	Gly	Ile	Asp	Phe	Ala	Leu	Ala	Ala	Leu	His	Thr
	225					230				235					240	
25	Trp	Asn	Lys	Met	Pro	Val	Ile	Glu	Val	Gln	Gly	Ile	Val	Pro	Thr	Glu
					245					250					255	
	Ile	Ile	Val	Ser	Pro	Arg	Tyr	Tyr	Arg	Met	Gly	Phe	Val	Gly	Gly	Asp
			260						265					270		
	Leu	Ser	Val	Pro	Val	Gly	Gln	Phe	Val	Phe	Arg	Gly	Glu	Ala	Ala	Phe
30			275						280					285		
	Asn	Ile	Asp	Lys	His	Phe	Thr	Tyr	Lys	Ser	His	Ala	Glu	Gln	Glu	Gly
			290						295					300		
	Phe	Gln	Thr	Ile	Asn	Trp	Leu	Ala	Gly	Ala	Asp	Trp	Tyr	Ala	Pro	Gly
	305				310					315					320	
35	Glu	Trp	Met	Ile	Ser	Gly	Gln	Phe	Ser	Met	Glu	Ser	Ile	Phe	Arg	Tyr
					325					330					335	

Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn
 340 345 350
 Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr
 355 360 365
 5 Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp
 370 375 380
 Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe
 385 390 395 400
 Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu
 10 405 410 415
 Leu Trp Phe Lys Ala Arg Tyr Ser Phe
 420 425

(2) INFORMATION FOR SEQ ID NO:133

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...211

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

Met Ser Ile Arg Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala
 35 1 5 10 15
 Gln Thr His Asp His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe

	20	25	30
	Gly Ala Ile Asp Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr		
	35	40	45
	Thr Ser Pro Thr His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg		
5	50	55	60
	Ser Tyr Gly Arg Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu		
	65	70	75 80
	His His His Ser Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro		
	85	90	95
10	Phe Asp Asn Ala Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile		
	100	105	110
	Arg Pro Ile Val Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His		
	115	120	125
	Leu Phe Phe Lys Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp		
15	130	135	140
	Asn Tyr Thr Val Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln		
	145	150	155 160
	Arg Ser His Thr His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu		
	165	170	175
20	Phe Asp Met Arg Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile		
	180	185	190
	Val Ala Asp Phe Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly		
	195	200	205
	Leu Asn His		
25	210		

(2) INFORMATION FOR SEQ ID NO:134

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

10

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Met Lys Leu Leu Leu Tyr Leu Leu Leu Val Leu Ser Thr Leu Ser Pro
1           5           10           15
Met Tyr Ser Gln Met Leu Phe Ser Glu Asn Leu Thr Met Asn Ile Asp
           20           25           30
15 Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu Pro Val Leu Asp Phe Lys
           35           40           45
Thr Glu Lys Glu Asn Val Phe Thr Phe Lys Asn Thr Ala Asn Leu Asn
           50           55           60
Leu Leu Ile Lys His Gly Gln Val Ile Asn Leu Ile Asn Lys Leu Glu
20 65           70           75           80
Phe Ser Thr Tyr Gly Asn Lys Val Thr Val Ser Gly Gly Tyr Val His
           85           90           95
Thr Glu Tyr Arg Tyr Leu Leu His His Val Phe Glu Val Tyr Pro Tyr
           100          105          110
25 Val Glu Ser Gln Trp Ala Glu Ser Arg Gly Met Lys Tyr Lys Val Ser
           115          120          125
Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val Asn Ser Asp Asn Cys Leu
           130          135          140
Met Phe Ala Thr Leu Gly Val Phe Phe Glu Phe Glu Lys Trp Glu Gln
30 145          150          155          160
Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr Ala Tyr Ser Arg Ser Ile
           165          170          175
Lys Ser His Leu Ser Ile Ser Phe Arg His Arg Leu Gly Glu His Trp
           180          185          190
35 Glu Phe Thr Thr Thr Ala Ile His Gln Gly Lys Pro Asp Ser Tyr Phe
           195          200          205

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Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp Leu Lys Tyr His Ile Thr
 210 215 220
 Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg Ile Ile Tyr Asp Thr Ala
 225 230 235 240
 5 Pro Ile Val Pro Val Arg Lys Asp Tyr Asn Thr Val Asp Val Gly Ile
 245 250 255
 Asp Ile Ser Phe
 260

10 (2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 25 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

30 Met Lys Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu
 1 5 10 15
 Thr Gly Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr
 20 25 30
 Ala Phe Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser
 35 35 40 45
 Ala Tyr Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Gly Ser Ile

	50		55		60
	Thr Arg Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu				
	65		70		75
	Asn Leu Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg				80
5		85		90	95
	Trp Met Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn				
		100		105	110
	Pro Ala Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala				
		115		120	125
10	Ala Ala Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met				
		130		135	140
	Asp Asn Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly				
		145		150	155
	Gly Ile Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu				160
15		165		170	175
	Tyr Thr Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser				
		180		185	190
	Glu Thr Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe				
		195		200	205
20	Gly Ile Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe				
		210		215	220
	Leu Leu Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly				
		225		230	235
	Lys Phe Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg				240
25		245		250	255
	Asn Phe Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser				
		260		265	270
	Ser Leu Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile				
		275		280	285
30	Gly Phe Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn				
		290		295	300
	Thr Gly Arg Arg Thr Ser Leu Tyr Tyr His Asp				
		305		310	315

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 776 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

15

(B) LOCATION 1...776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu
 20 1 5 10 15
 Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn
 20 25 30
 Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys
 35 40 45
 25 Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu
 50 55 60
 Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp
 65 70 75 80
 Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val
 30 85 90 95
 Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg
 100 105 110
 Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys
 115 120 125
 35 Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly
 130 135 140

Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp
 435 440 445
 Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile
 450 455 460
 5 Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro
 465 470 475 480
 Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn
 485 490 495
 Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg
 10 500 505 510
 Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser
 515 520 525
 Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala
 530 535 540
 15 Ala Ile Gly His Lys Thr Ile Tyr Ala Met Ala Val Asp His Asn Gly
 545 550 555 560
 Ser Val Trp Met Gly Ser Asp Ile Gly Ile Phe Gly Val Tyr Asn Ala
 565 570 575
 Ala Gly Val Leu Ser Ser Thr Ser Thr Pro Ile Ala Val Arg Pro Val
 20 580 585 590
 Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val
 595 600 605
 Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln
 610 615 620
 25 Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala
 625 630 635 640
 Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser
 645 650 655
 Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp
 30 660 665 670
 Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu
 675 680 685
 Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro
 690 695 700
 35 Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile
 705 710 715 720

	Gly	Phe	Gly	Leu	Ser	Val	Leu	Asp	Val	Ala	Glu	Ala	Arg	Ile	Pro	Ala	
	145						150				155					160	
	Thr	Tyr	Ala	Lys	Gly	Thr	Lys	Val	Thr	Asp	Val	Ala	Lys	Leu	Asp	Asn	
					165					170					175		
5	Asp	Arg	Leu	Leu	Met	Leu	Lys	Glu	Gly	Gln	Leu	Phe	Ile	Gly	Lys	Glu	
				180					185					190			
	Thr	Asp	Asn	Leu	Gln	Asp	Pro	Ala	Ala	Trp	Thr	Ala	Leu	Ser	Leu	Asn	
			195					200					205				
	Leu	Pro	Met	Gly	Ser	Val	Thr	Gly	Leu	Gly	Ile	Val	Gly	Glu	Asp	Ile	
10		210					215					220					
	Cys	Phe	Leu	Leu	Ala	Asp	Gly	Arg	Val	Tyr	Val	Ala	Ala	Asn	Gln	Ser	
	225					230				235						240	
	Phe	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Ser	Ser	Ala	Asp	Ser	Arg	Leu	Tyr	
				245					250						255		
15	Val	Thr	Asp	Arg	Gly	Leu	Phe	Ile	Cys	Ala	Glu	Asn	Arg	Ile	Tyr	Phe	
				260					265					270			
	Ile	Glu	Lys	Gly	Arg	Lys	Thr	Thr	Gln	Phe	Pro	Ile	Ala	Asp	Val	Leu	
			275					280					285				
	Gly	Val	Gly	Ala	Met	Asn	Glu	Ser	Asn	Thr	Ala	Tyr	Ile	Ala	Leu	Gly	
20		290					295					300					
	Glu	Glu	Gly	Leu	Ala	Ser	Leu	Leu	Leu	Ala	Glu	Gly	Ser	Thr	Ala	Glu	
	305					310					315					320	
	Ala	Met	Pro	Val	Ala	Phe	Asp	Gly	Pro	Gly	Asp	Asn	Asp	Phe	Tyr	Glu	
				325					330						335		
25	Met	Arg	Phe	Ser	His	Gly	Arg	Leu	Tyr	Ala	Ala	Ser	Gly	Leu	Trp	Gly	
			340					345						350			
	Thr	Asn	Leu	Met	Gly	His	Ala	Gly	Met	Val	Lys	Leu	Tyr	Asp	Gly	Asn	
			355					360					365				
	Arg	Trp	Thr	Asn	Phe	Asp	Lys	Lys	Thr	Val	Gln	Glu	Gln	Leu	Gly	Gly	
30		370					375					380					
	Gly	Phe	Ser	Phe	Asn	Asp	Ala	Ile	Asp	Ile	Ala	Val	Ser	Asn	Gly	Asp	
	385					390					395					400	
	Pro	Asp	His	Phe	Phe	Val	Gly	Thr	Trp	Gly	Asn	Gly	Leu	Phe	Glu	Phe	
				405					410						415		
35	Lys	Asp	Gly	Lys	Ala	Ile	Ala	Arg	Tyr	Ser	Gly	Asn	Glu	Thr	Ala	Ile	
			420					425					430				

Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr
 725 730 735
 Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser
 740 745 750
 5 Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Lys Ser Lys
 755 760 765
 Leu Ile Arg Phe Ala Val Ile Arg
 770 775

10 (2) INFORMATION FOR SEQ ID NO:137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 25 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

30 Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu
 1 5 10 15
 Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Glu Cys
 20 25 30
 Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala
 35 35 40 45
 Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe

	50	55	60
	Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg		
	65	70	75 80
	Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn		
5	85	90	95
	Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln		
	100	105	110
	Ser Val Tyr Arg Leu Arg Met Ala His Ala Arg Arg Glu Ala Ser Arg		
	115	120	125
10	Leu Ser Val Arg Glu Gln Gln Glu Leu Ala Ala Leu Gly Thr Thr Glu		
	130	135	140
	Ala Tyr Tyr Asp Leu Val Tyr Ala Arg Gln Met Gln Glu Leu Ala Met		
	145	150	155 160
	Gln Lys Tyr Glu Glu Ser Ser Arg Leu His Arg Gln Thr Ala Arg Met		
15	165	170	175
	Glu Glu Leu Gly Met Lys Ser Arg Pro Asp Val Leu Glu Met Gln Ser		
	180	185	190
	Arg Met Ala Gly Asp Arg Leu Ala Leu Thr Gln Ala Asp Asn Gln Cys		
	195	200	205
20	Ile Ile Ala Leu Ile Arg Leu Lys Glu Lys Met Asn Phe Pro Ile Asp		
	210	215	220
	Asp Glu Leu Val Val Asp Asp Met Pro Ala Asp Ser Leu Ser Ala Asp		
	225	230	235 240
	Met Ala Glu Ser Asp Ser Ser Ala Gly Val Phe Ala Arg Ala Ala His		
25	245	250	255
	His His Pro Val Leu Leu Arg Ala Lys Leu Asp Glu Gln Ala Ala Thr		
	260	265	270
	Asp Arg Leu Arg Ala Ala Arg Gly Ala Phe Leu Pro Ser Val Ser Val		
	275	280	285
30	Ser Gly Gly Trp Asn Thr Gly Phe Ser Arg Phe Leu Asn Gly Ser Asp		
	290	295	300
	Tyr Thr Pro Phe Ser Glu Gln Phe Arg Asn Arg Arg Gly Glu Tyr Val		
	305	310	315 320
	Ser Leu Asn Leu Ser Ile Pro Ile Phe Ser Gly Phe Ser Leu Val Ser		
35	325	330	335
	Leu Arg Gln Ala Arg Ala Glu Arg Arg Ala Ala Ile Val Arg Arg		

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340 345 350
Gly Glu Ala Glu Arg Arg Leu Tyr Ser Glu Ile Ala Gln Ala Met Ala
355 360 365
Asp Arg Asp Ala Ala Leu Ala Ser Tyr Arg Gln Ala Lys Glu His Thr
5 370 375 380
Asp Ala Met Gln Thr Ala Tyr Glu Ala Val Leu Gln Arg Tyr Glu Glu
385 390 395 400
Gly Leu Asn Thr Ala Ile Asp Leu Thr Thr Gln Ala Asn Arg Leu Leu
405 410 415
10 Asp Ala Arg Val Gln Arg Leu Arg Ala Ala Met Thr Tyr Arg Leu Lys
420 425 430
Cys Lys Leu Ile Ala Tyr Tyr Gly Cys Leu Ser Asp
435 440

15

